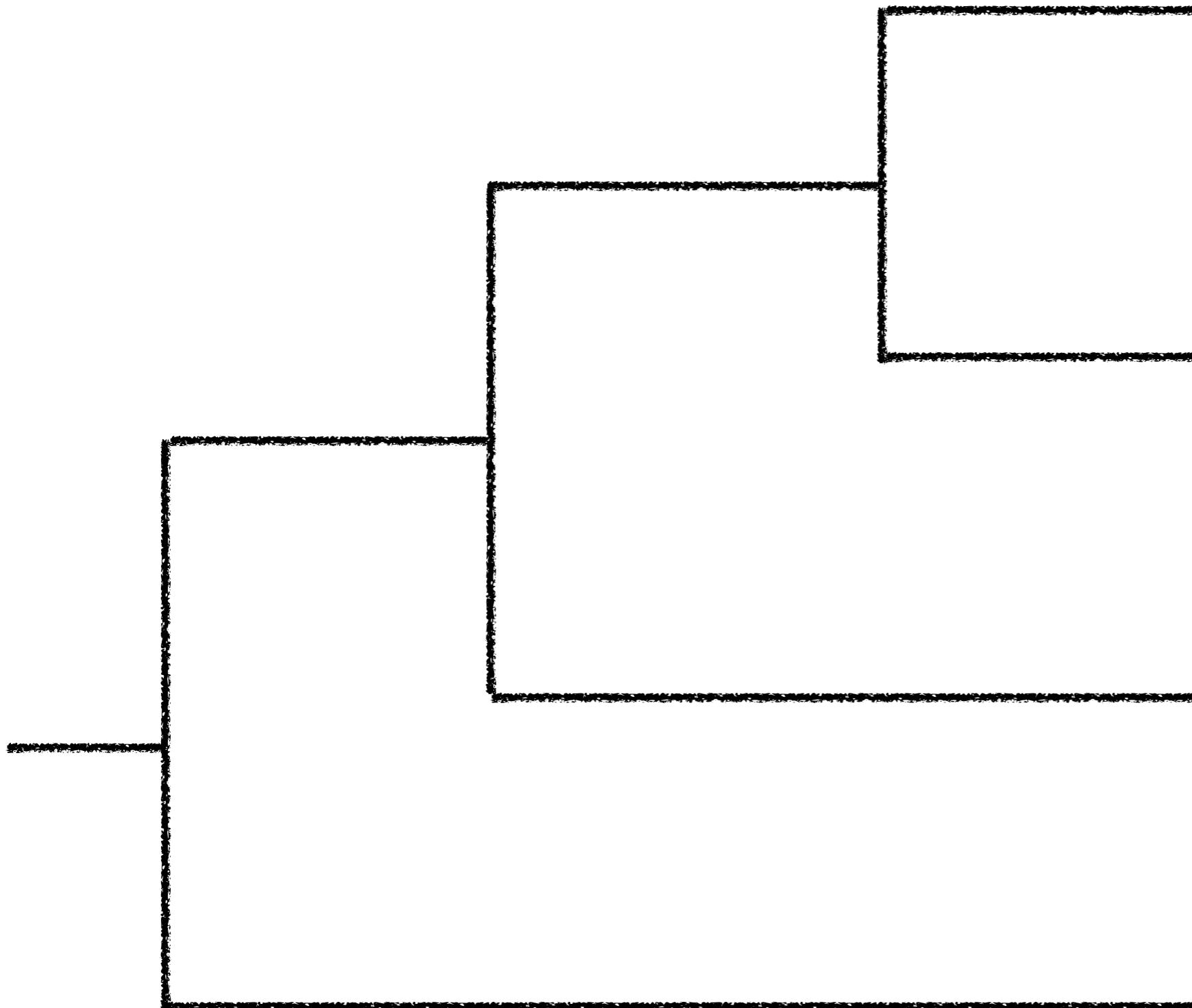


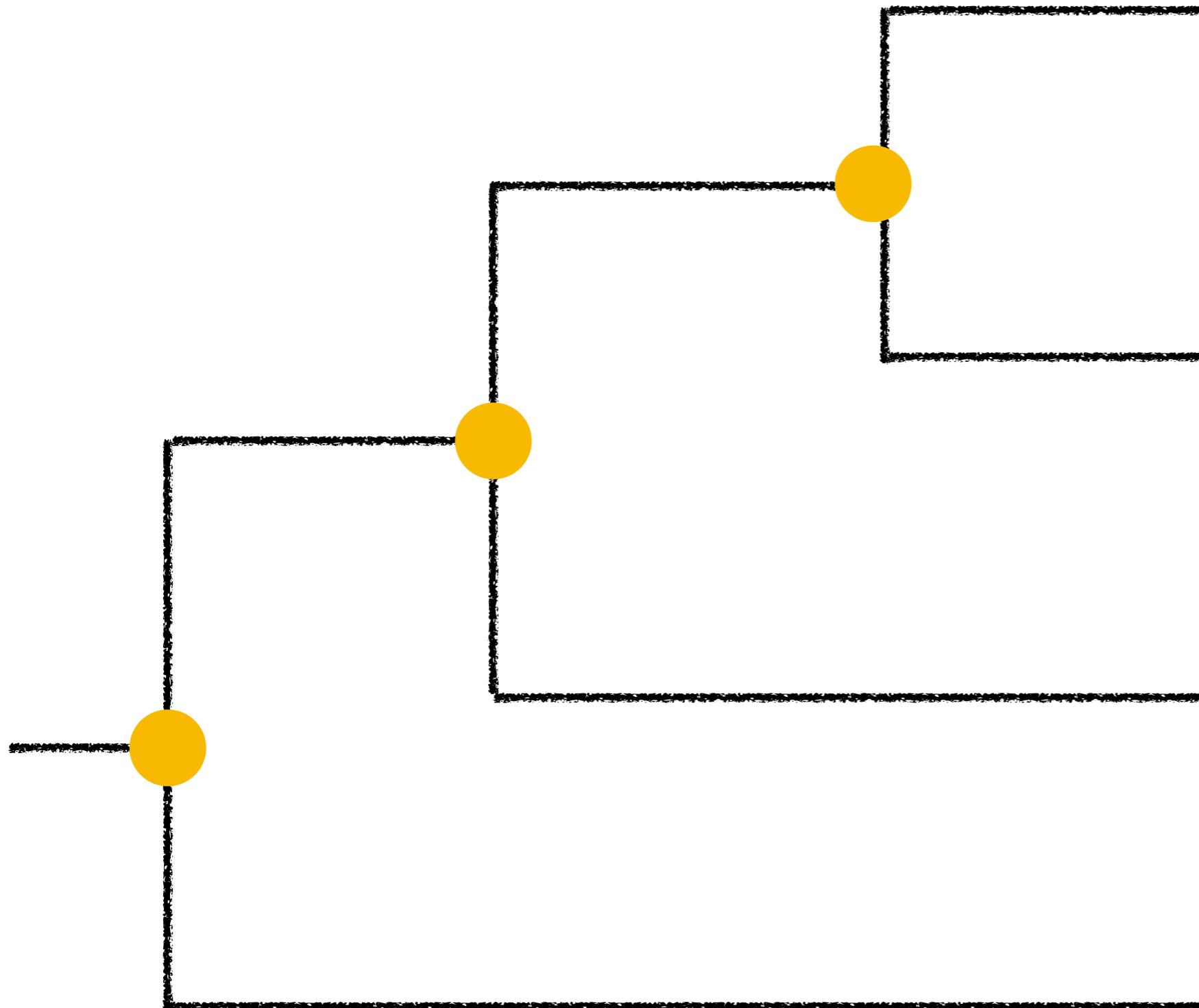
Lecture 7

Overview of phylogenetic inference
Botany 563 – Spring 2021

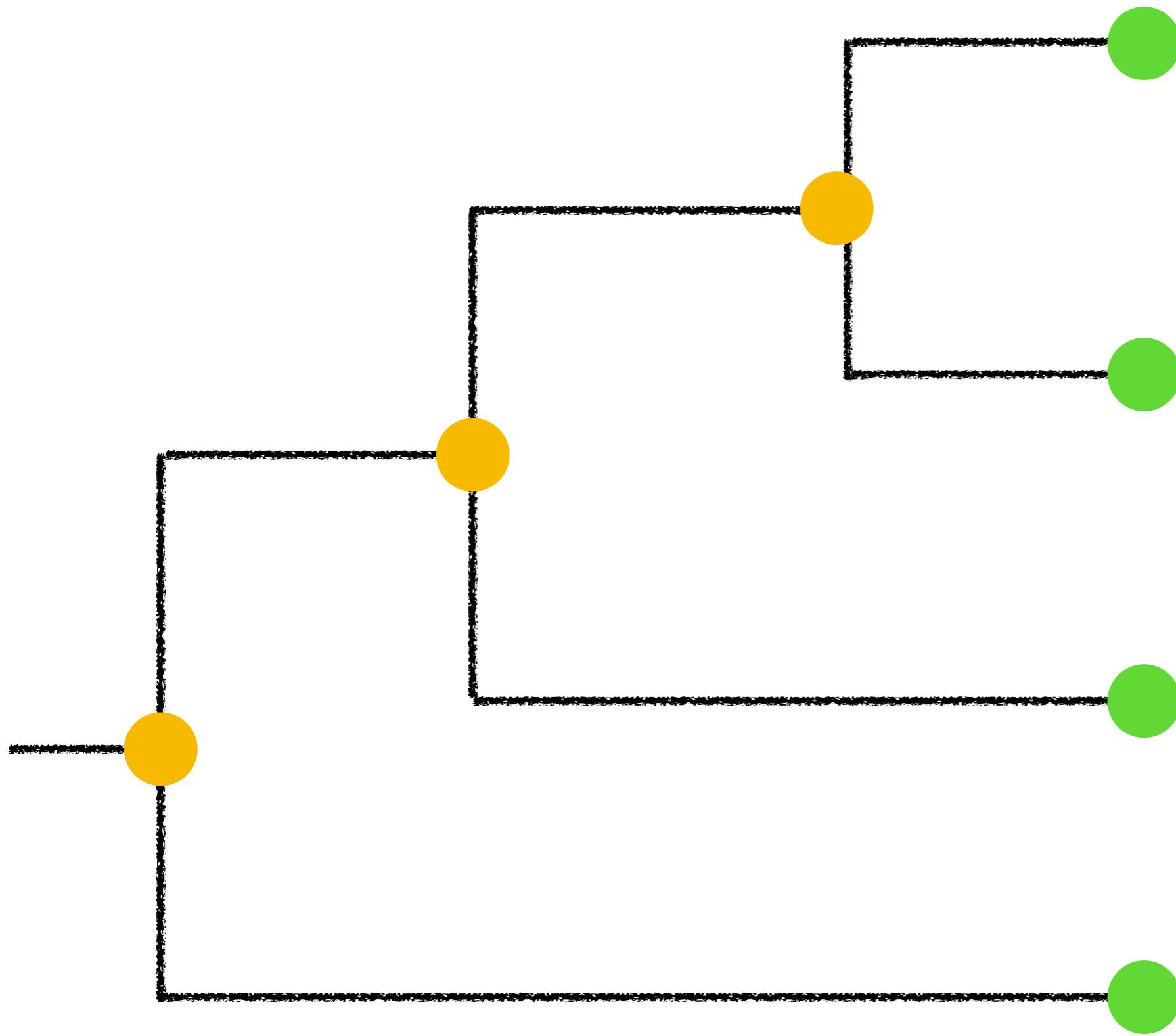
Phylogenetic tree



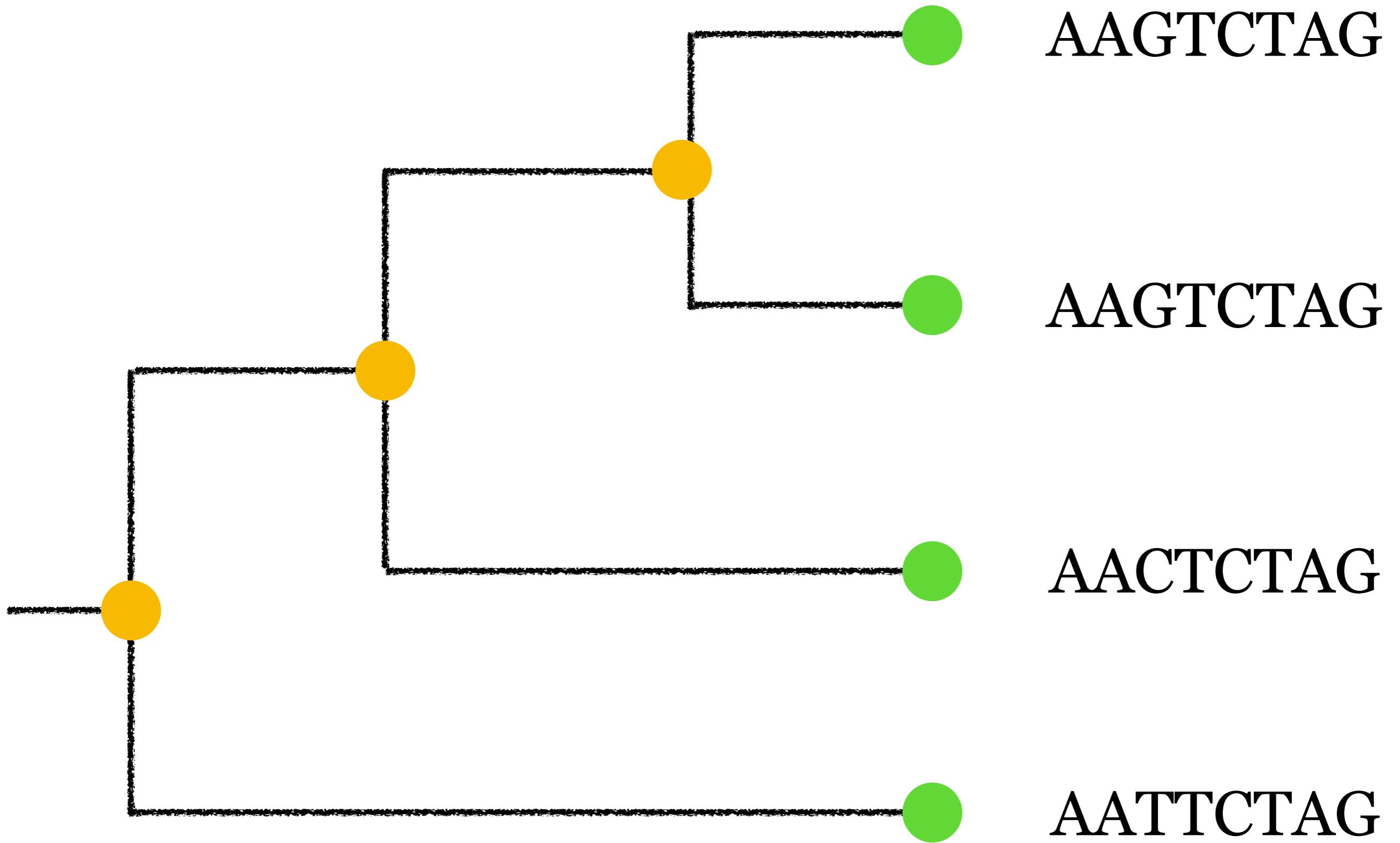
Phylogenetic tree



Phylogenetic tree

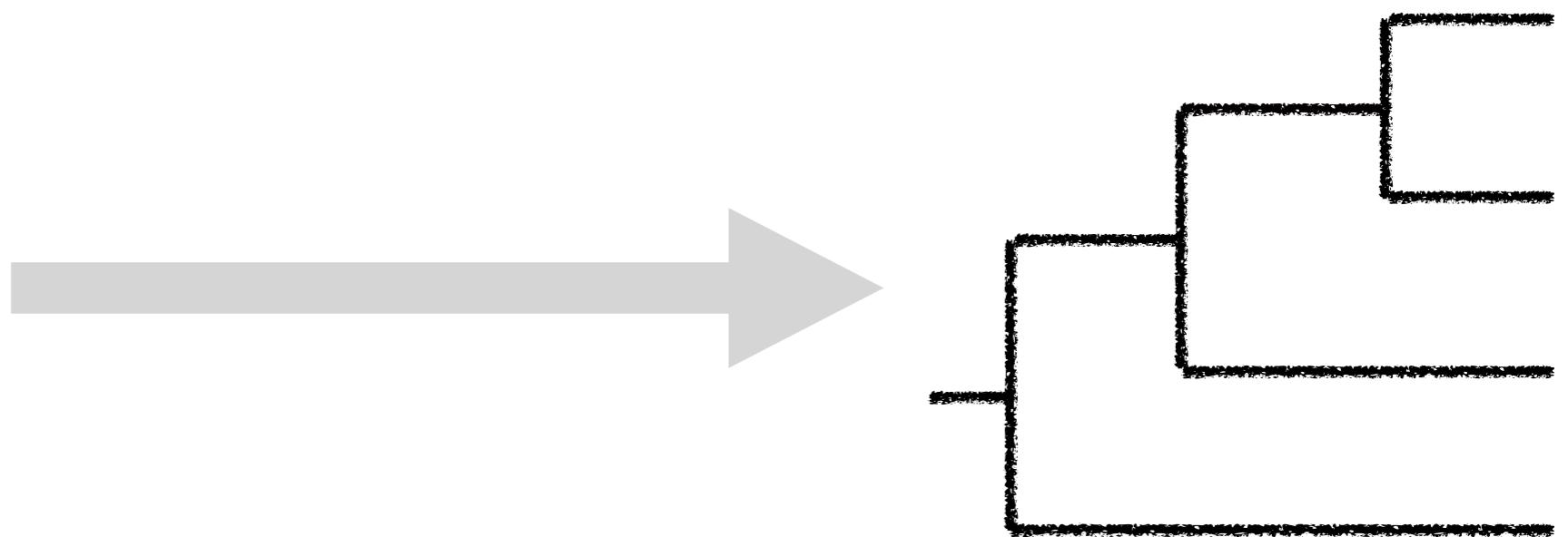


Phylogenetic tree

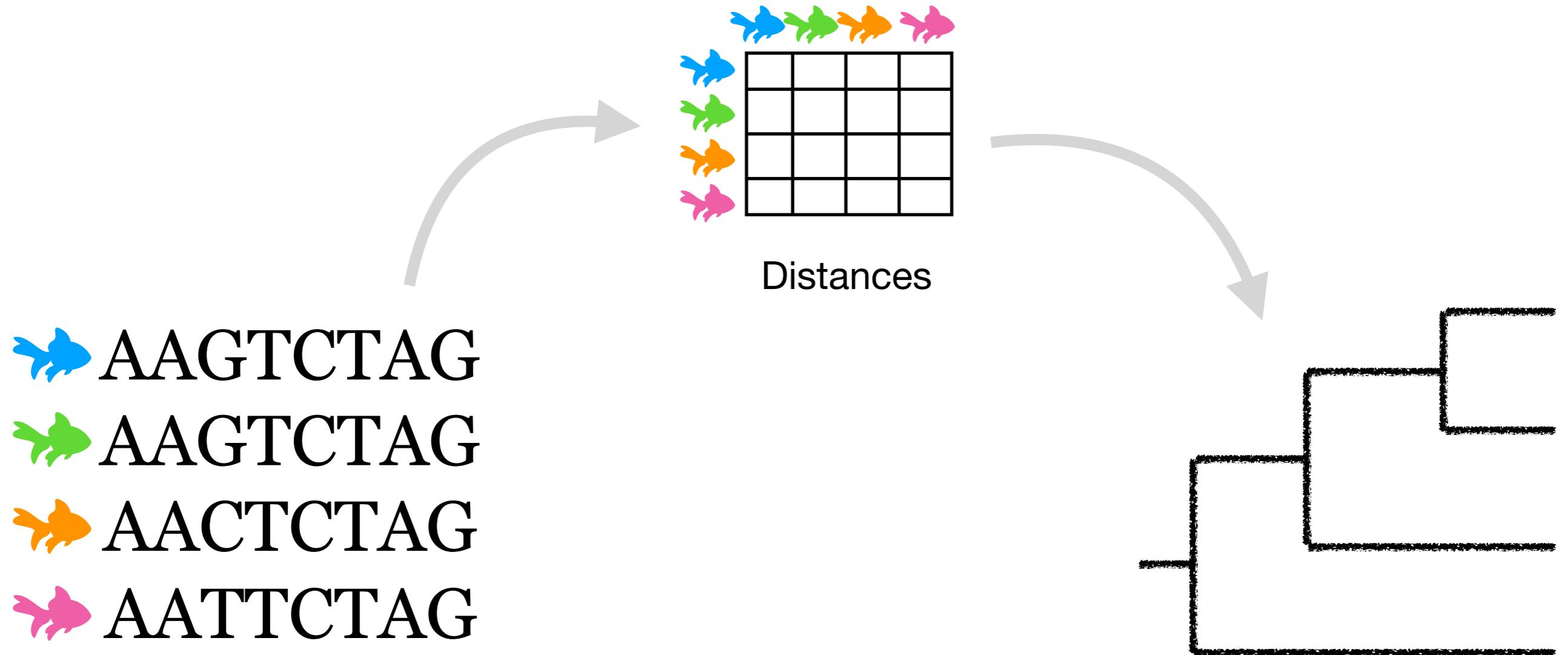


Phylogenetic inference

AAGTCTAG
AAGTCTAG
AACTCTAG
AATTCTAG

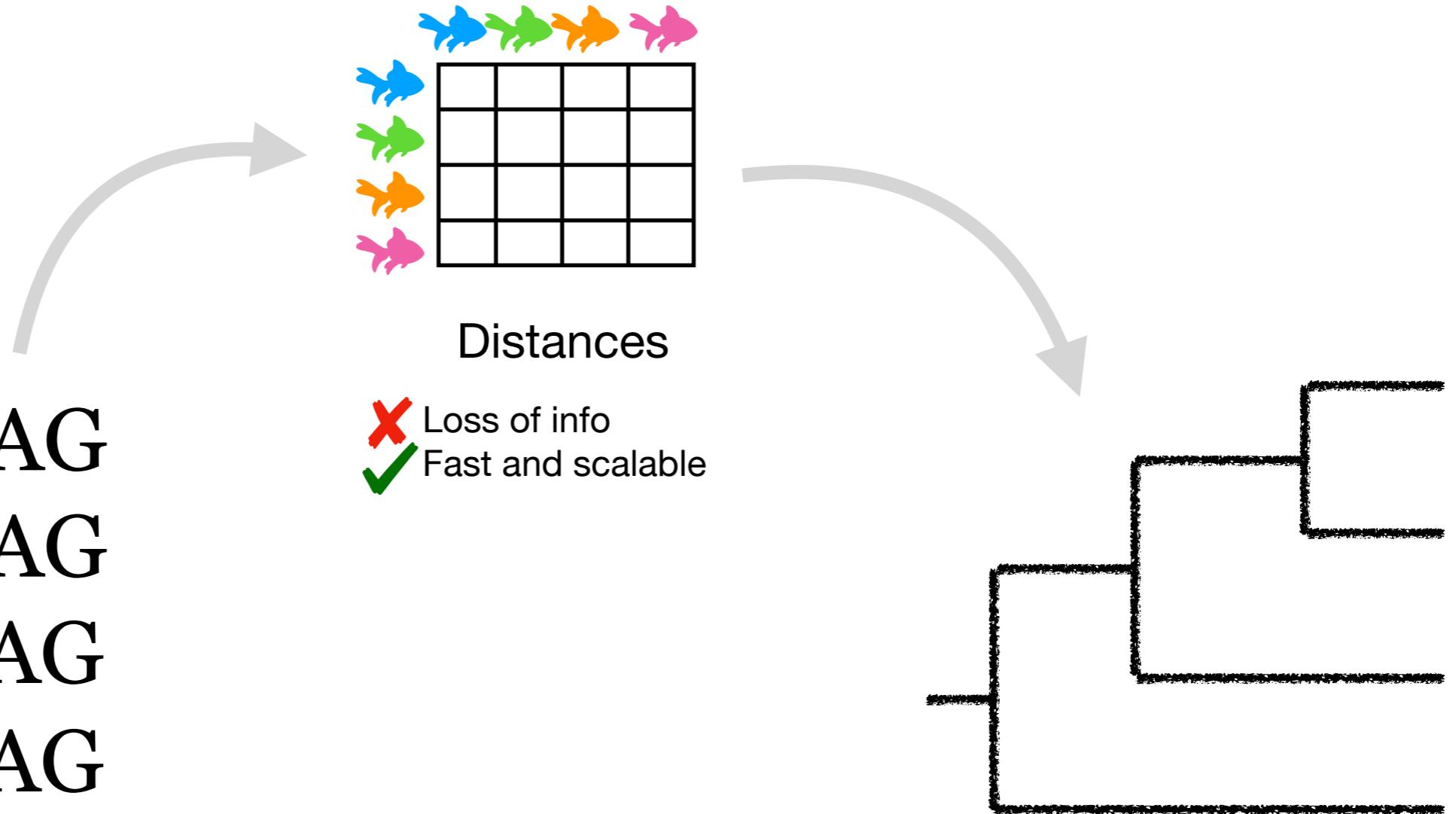


Phylogenetic inference

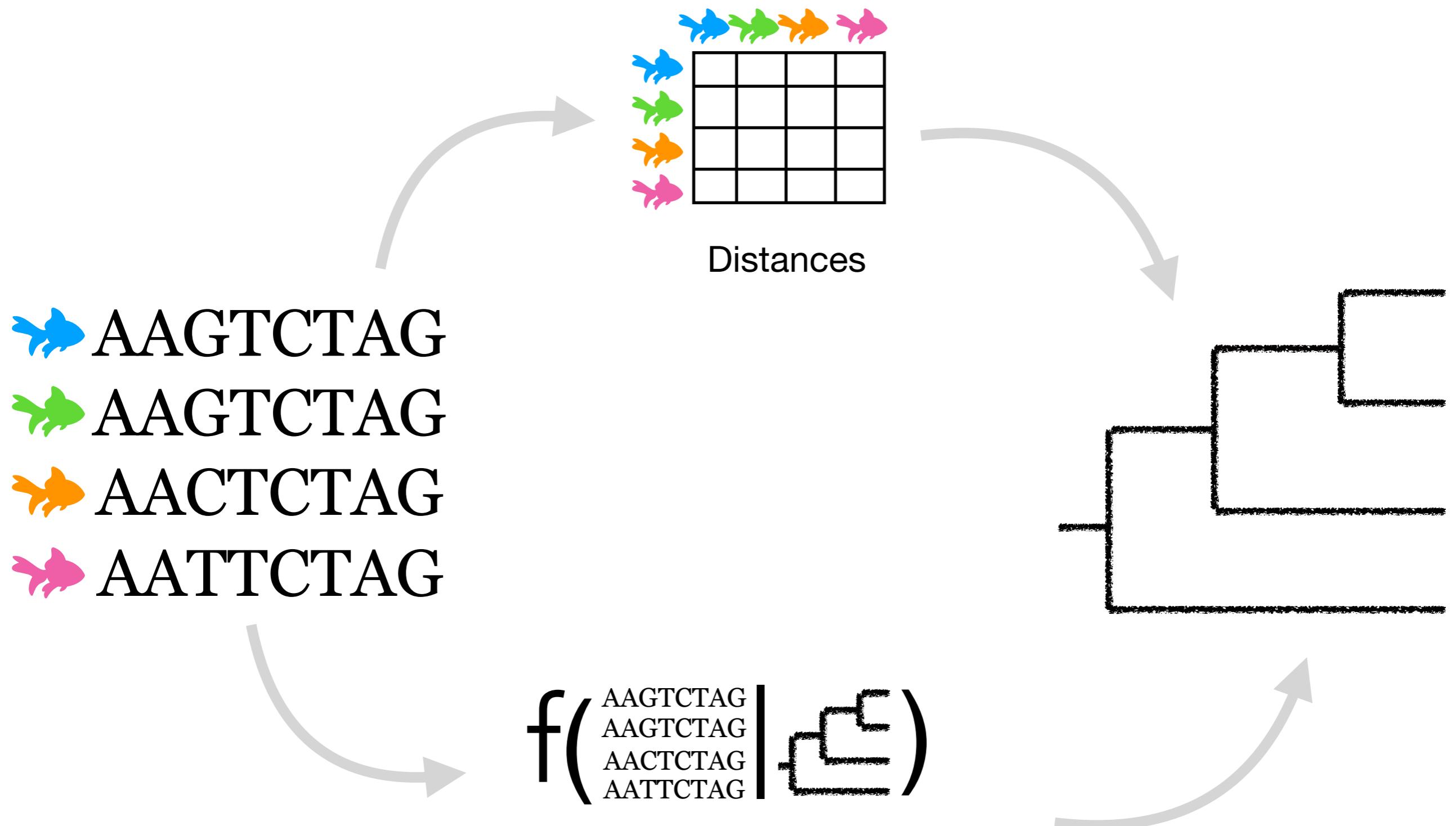


Phylogenetic inference

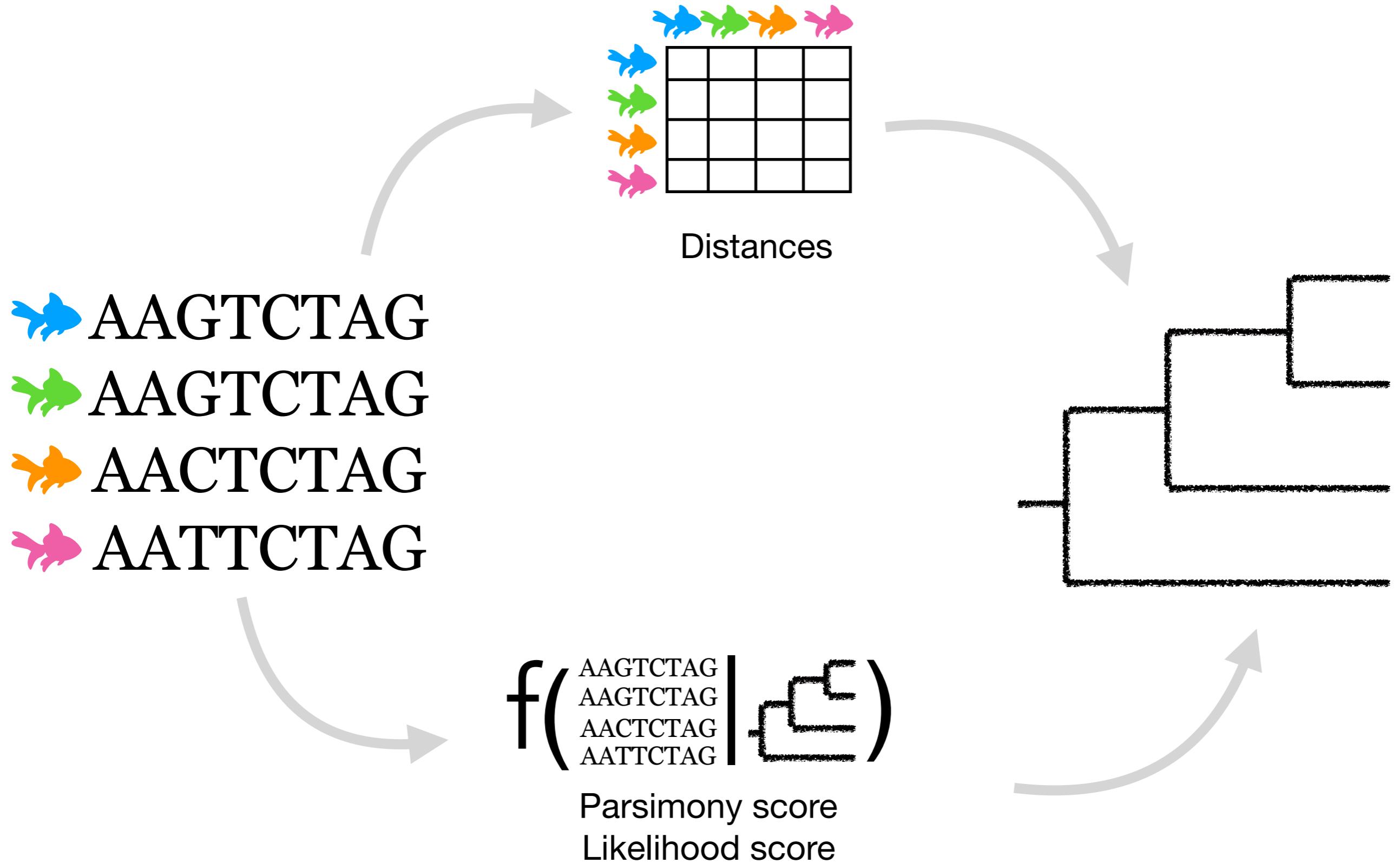
fish AAGTCTAG
fish AAGTCTAG
fish AACTCTAG
fish AATTCTAG



Phylogenetic inference

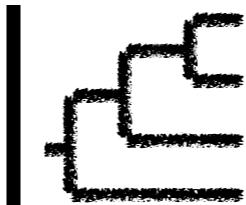


Phylogenetic inference



Phylogenetic inference

 AAGTCTAG
 AAGTCTAG
 AACTCTAG
 AATTCTAG

$f($ AAGTCTAG | )
Parsimony score
Likelihood score



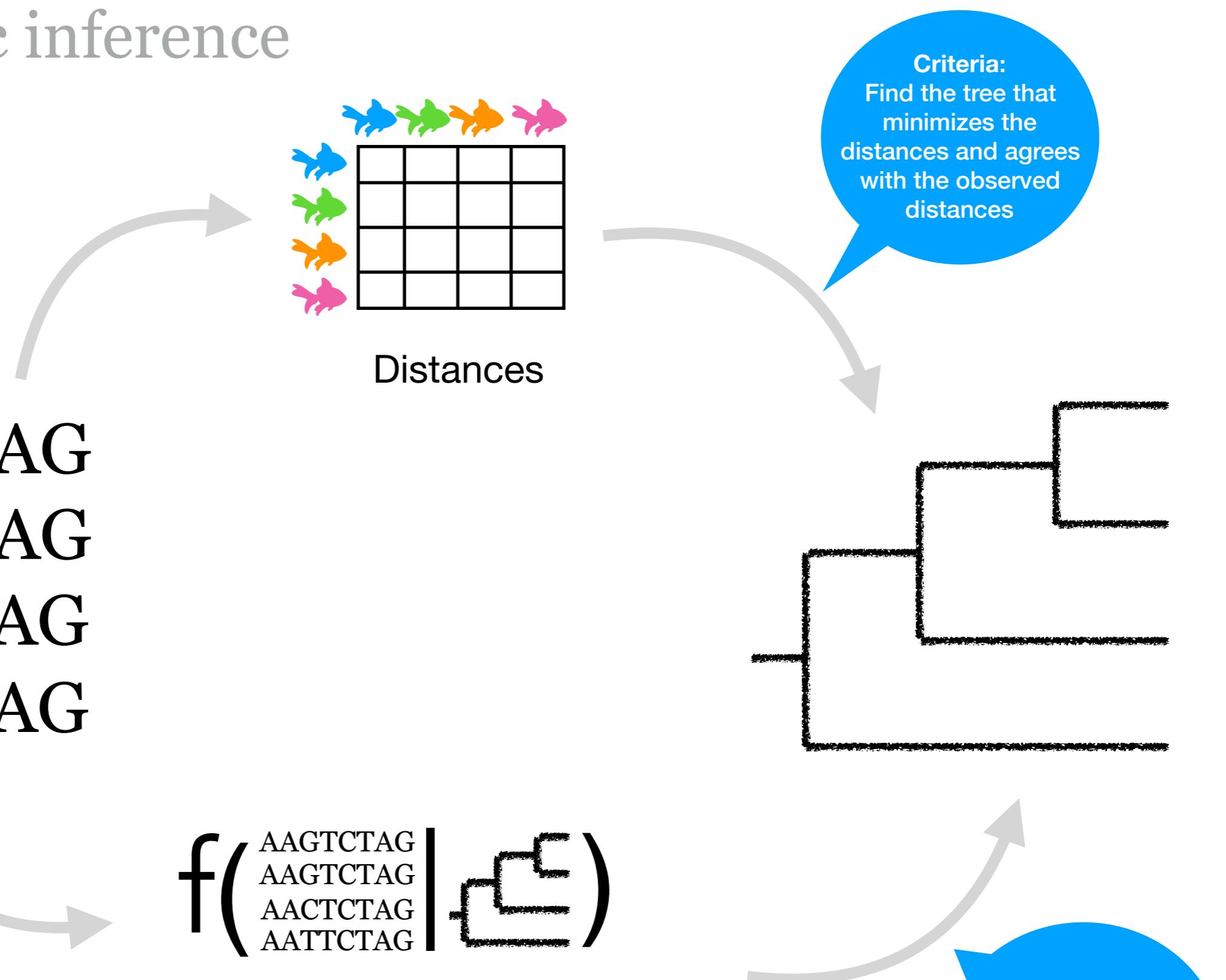
<https://solislemuslab.github.io/>



@solislemuslab



crsl4

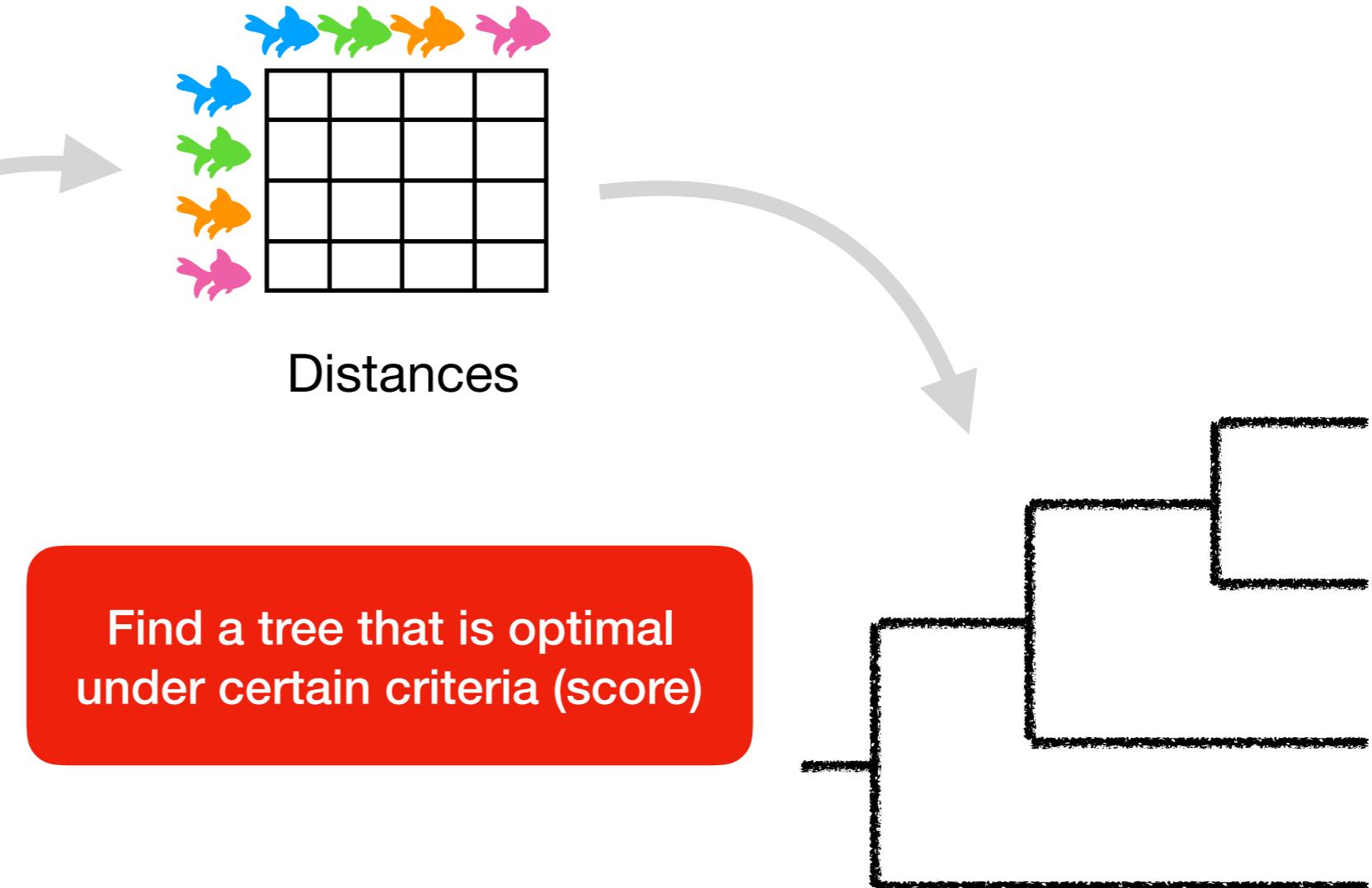


Criteria:
Find the tree that
minimizes the
distances and agrees
with the observed
distances

Criteria:
Find the tree that
maximizes the fit to the
data based on the
score

Phylogenetic inference

 AAGTCTAG
 AAGTCTAG
 AACTCTAG
 AATTCTAG



$f(AAGTCTAG | \text{tree})$

Parsimony score
Likelihood score

Phylogenetic inference

Step 1: Choose the criterion to use:
distances, parsimony, likelihood

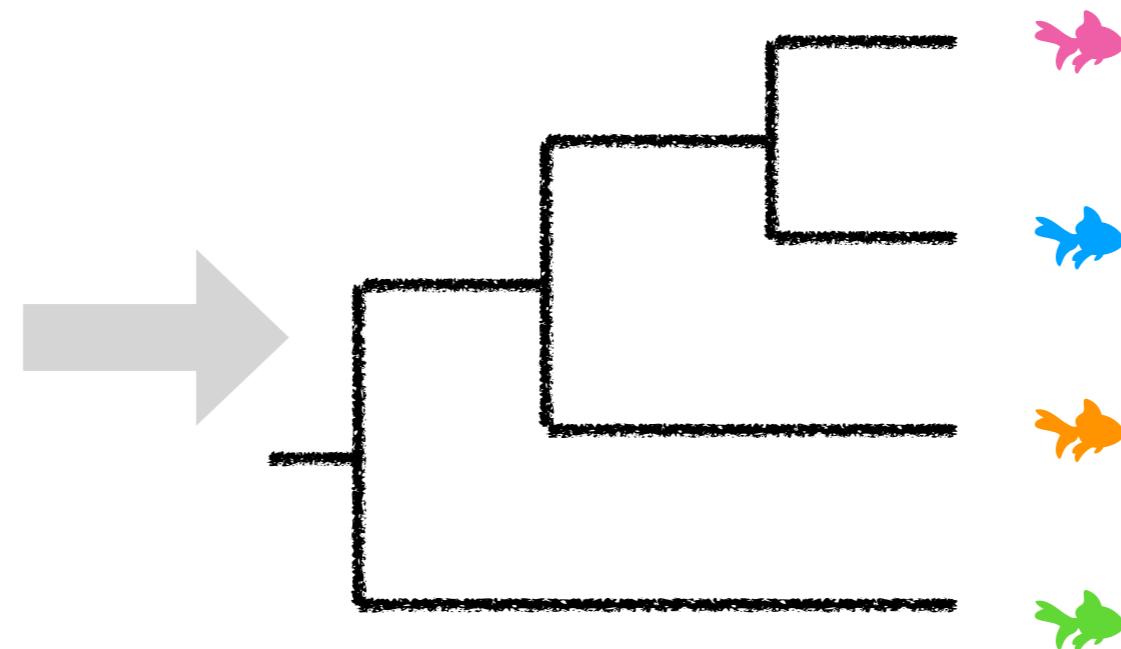
🐟 AAGTCTAG
🐠 AAGTCTAG
🐠 AACTCTAG
🐠 AATTCTAG

Phylogenetic inference

Step 1: Choose the criterion to use:
distances, parsimony, likelihood

Step 2: Guess the tree

🐟 AAGTCTAG
🐠 AAGTCTAG
🐡 AACTCTAG
🐙 AATTCTAG



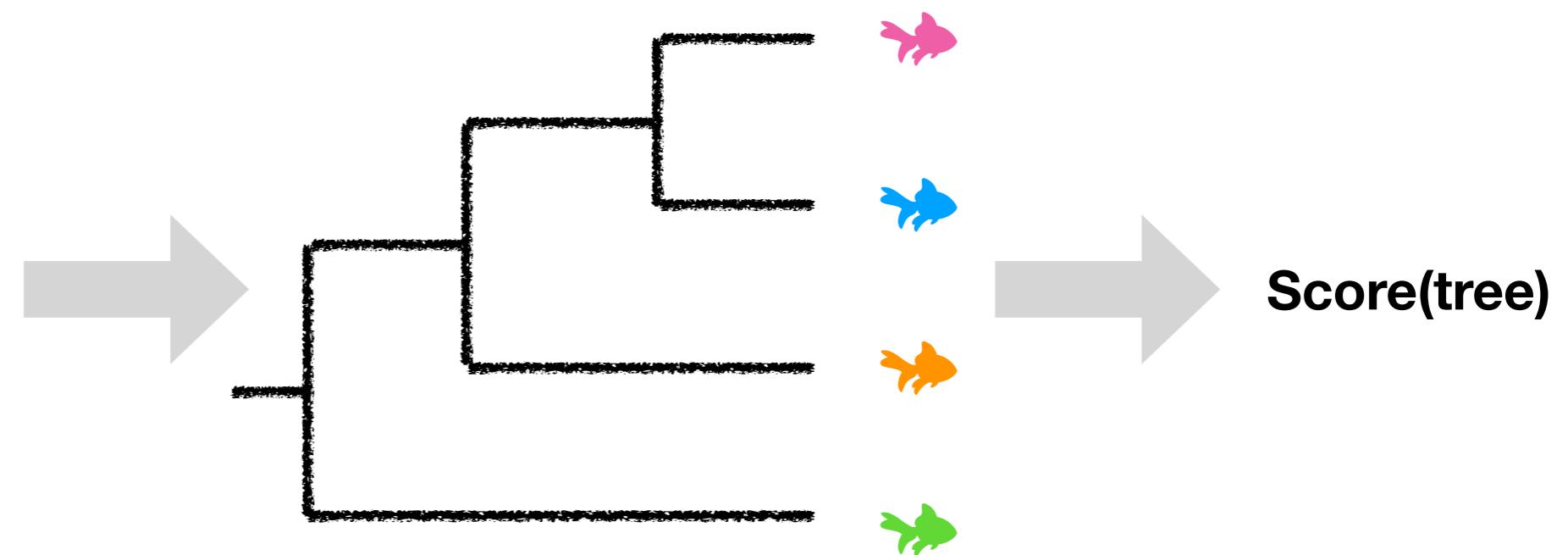
Phylogenetic inference

Step 1: Choose the criterion to use:
distances, parsimony, likelihood

Step 2: Guess the tree

Step 3: Evaluate the score of the
tree

🐟 AAGTCTAG
🐠 AAGTCTAG
🐡 AACTCTAG
🐙 AATTCTAG



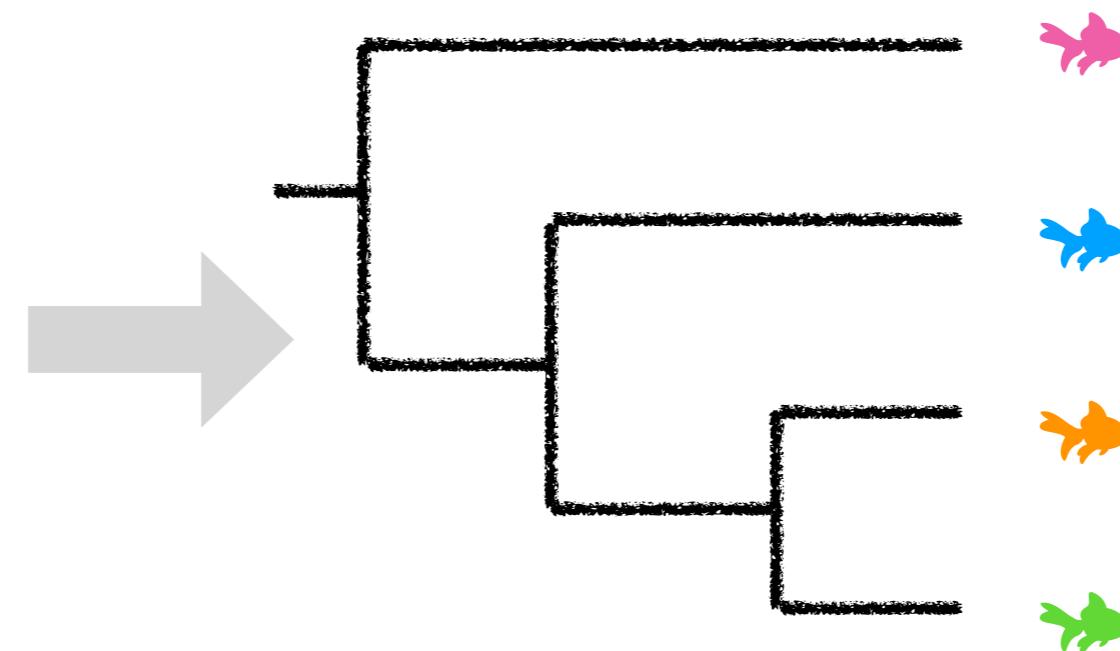
Phylogenetic inference

Step 1: Choose the criterion to use:
distances, parsimony, likelihood

Step 2: Guess the tree

Step 3: Evaluate the score of the
tree

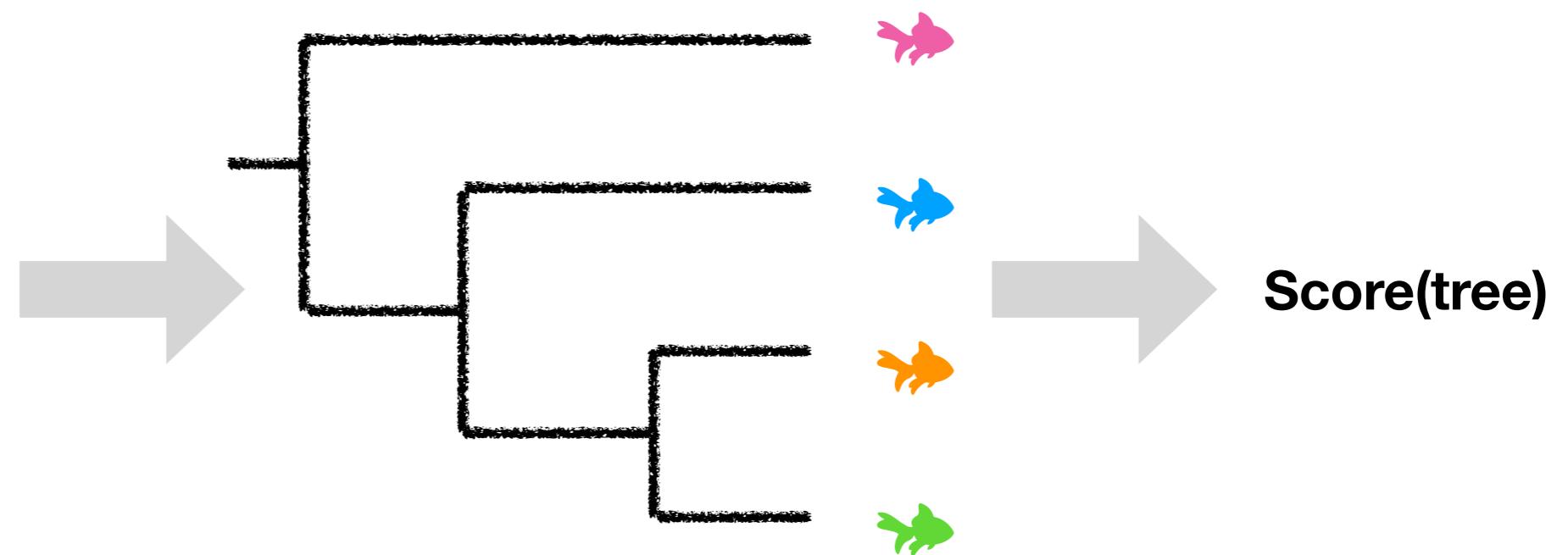
🐟 AAGTCTAG
🐠 AAGTCTAG
🐡 AACTCTAG
🐠 AATTCTAG



Step 4: Propose new tree

Phylogenetic inference

fish AAGTCTAG
fish AAGTCTAG
fish AACTCTAG
fish AATTCTAG



Step 1: Choose the criterion to use:
distances, parsimony, likelihood

Step 2: Guess the tree

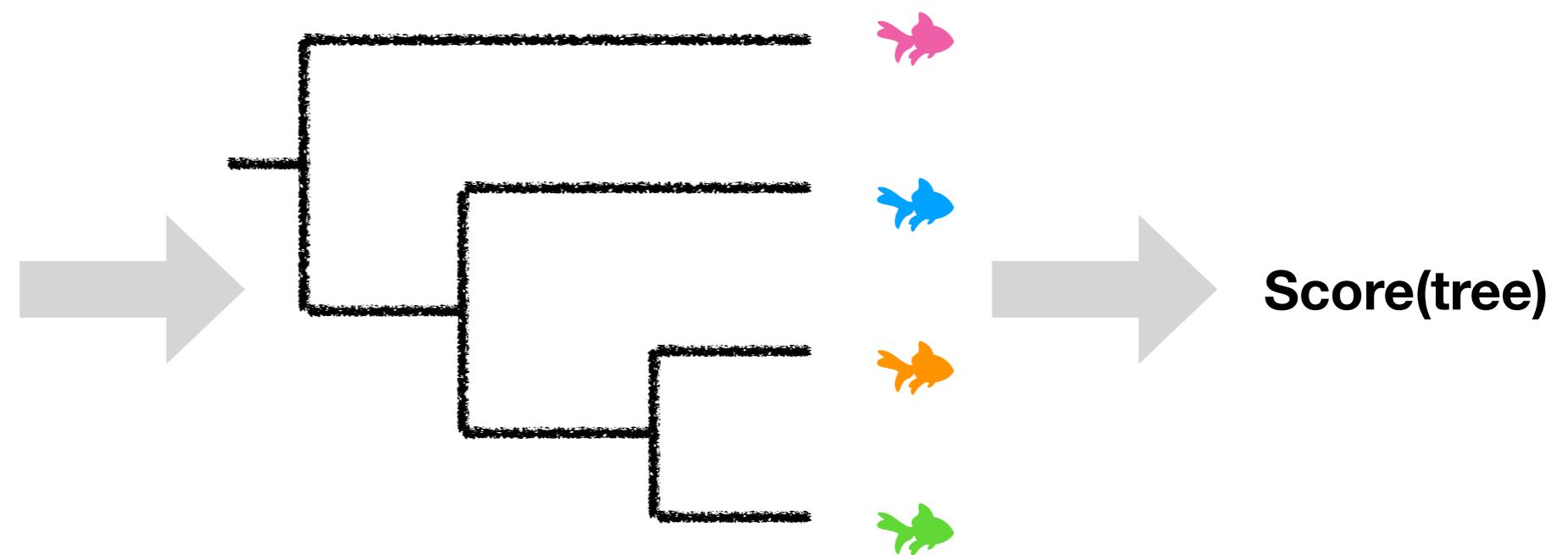
Step 3: Evaluate the score of the
tree

Step 4: Propose new tree

Step 5: Evaluate the score of the
tree

Phylogenetic inference

fish AAGTCTAG
fish AAGTCTAG
fish AACTCTAG
fish AATTCTAG



Step 1: Choose the criterion to use:
distances, parsimony, likelihood

Step 2: Guess the tree

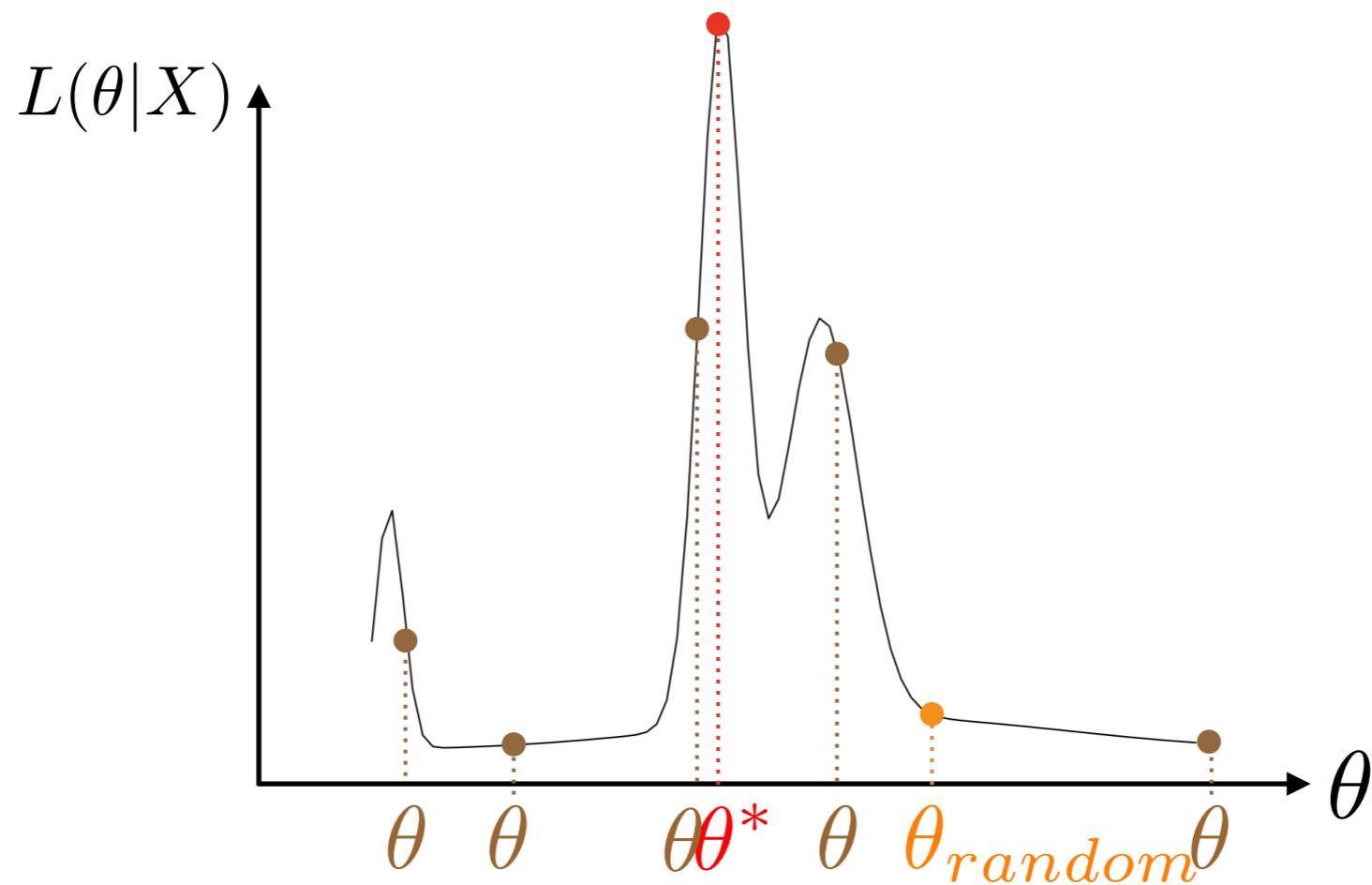
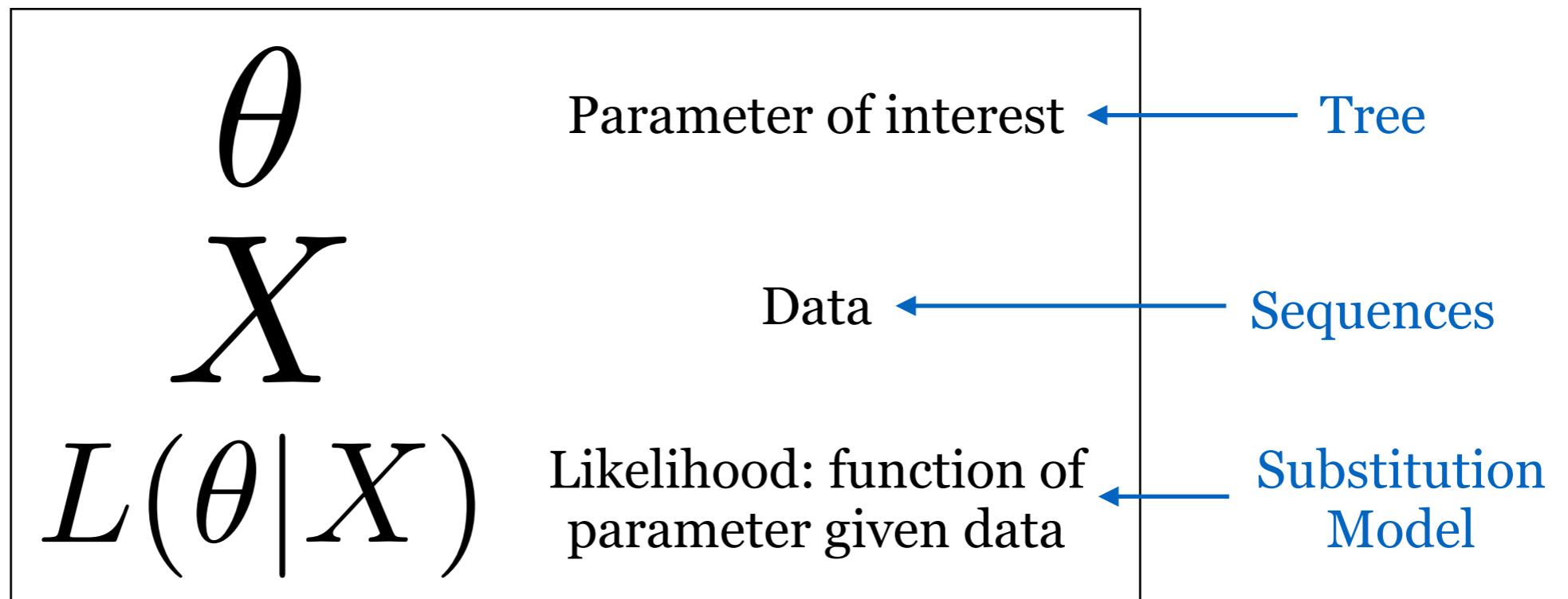
Step 3: Evaluate the score of the
tree

Step 4: Propose new tree

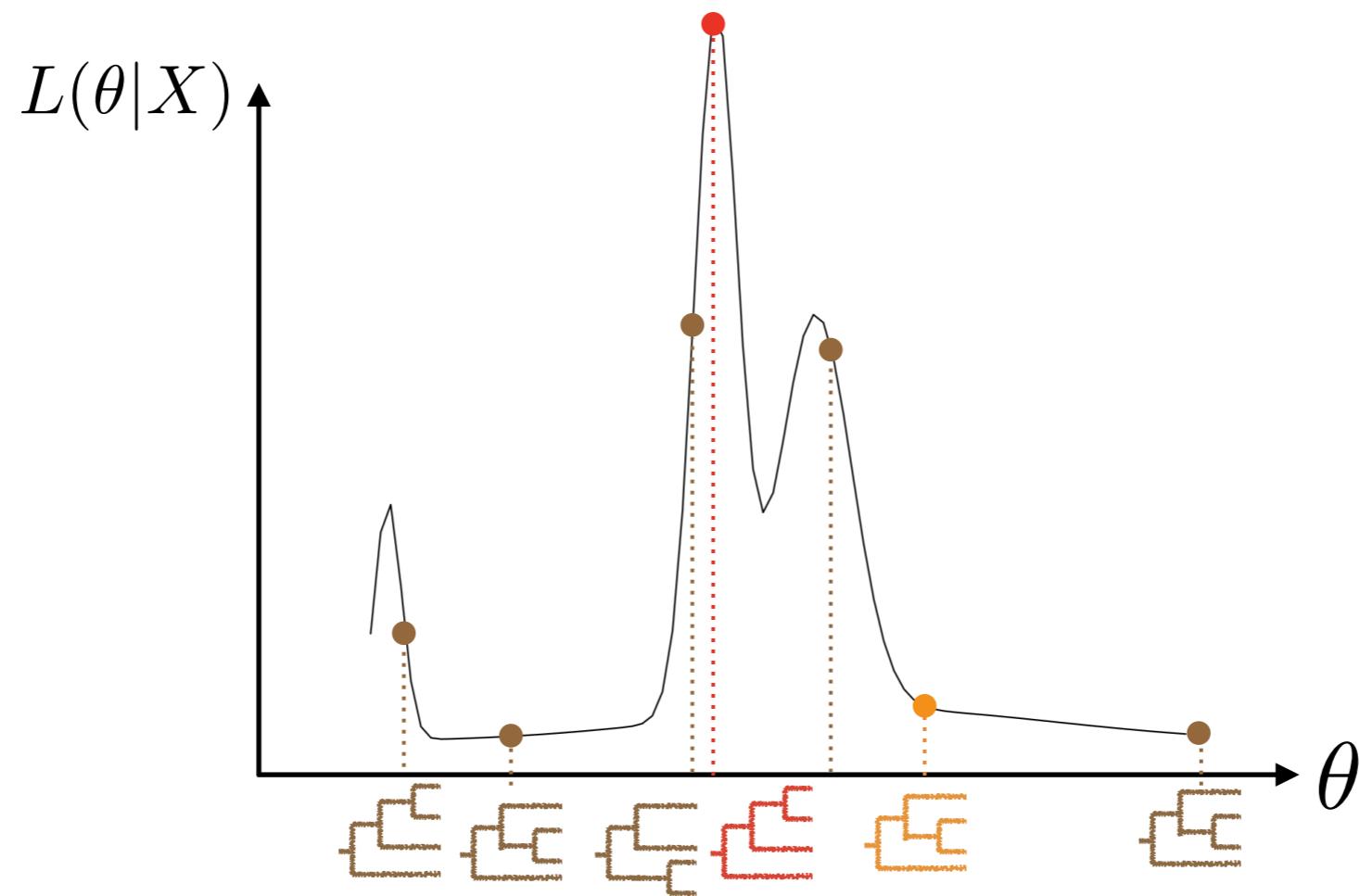
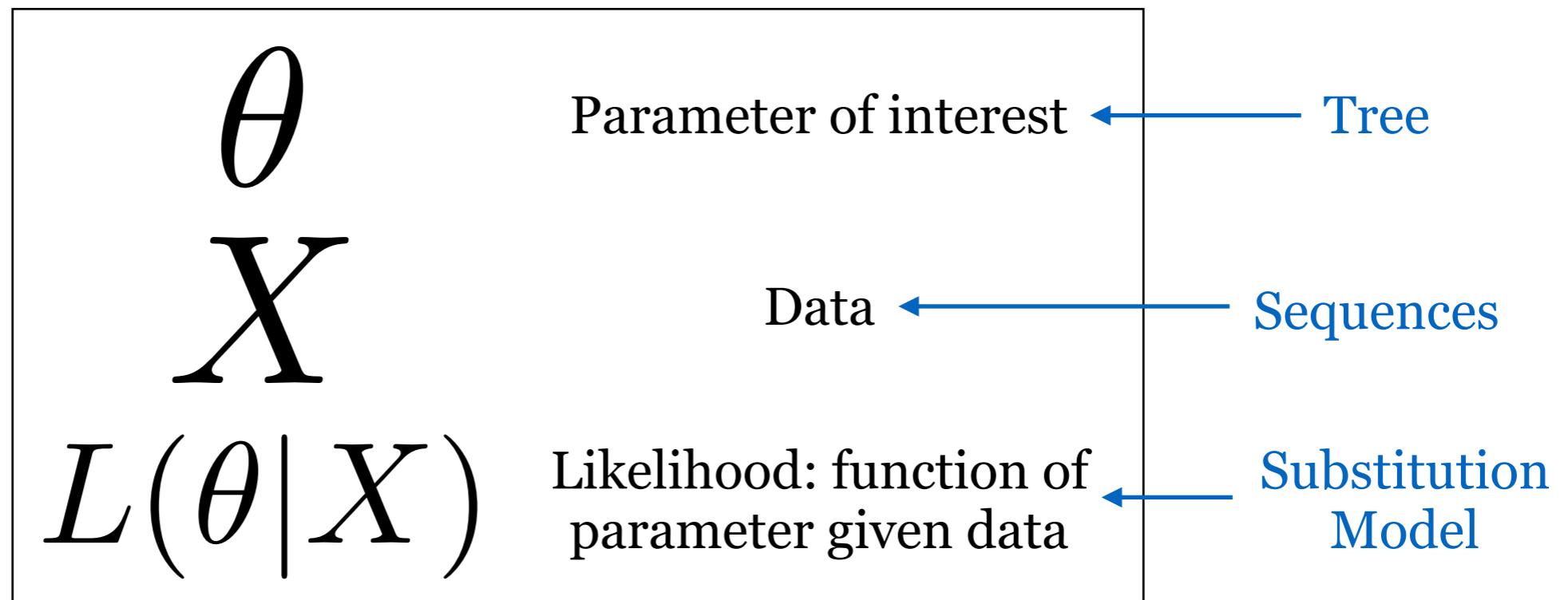
Step 5: Evaluate the score of the
tree

Continue until you scored all trees
and found the optimum

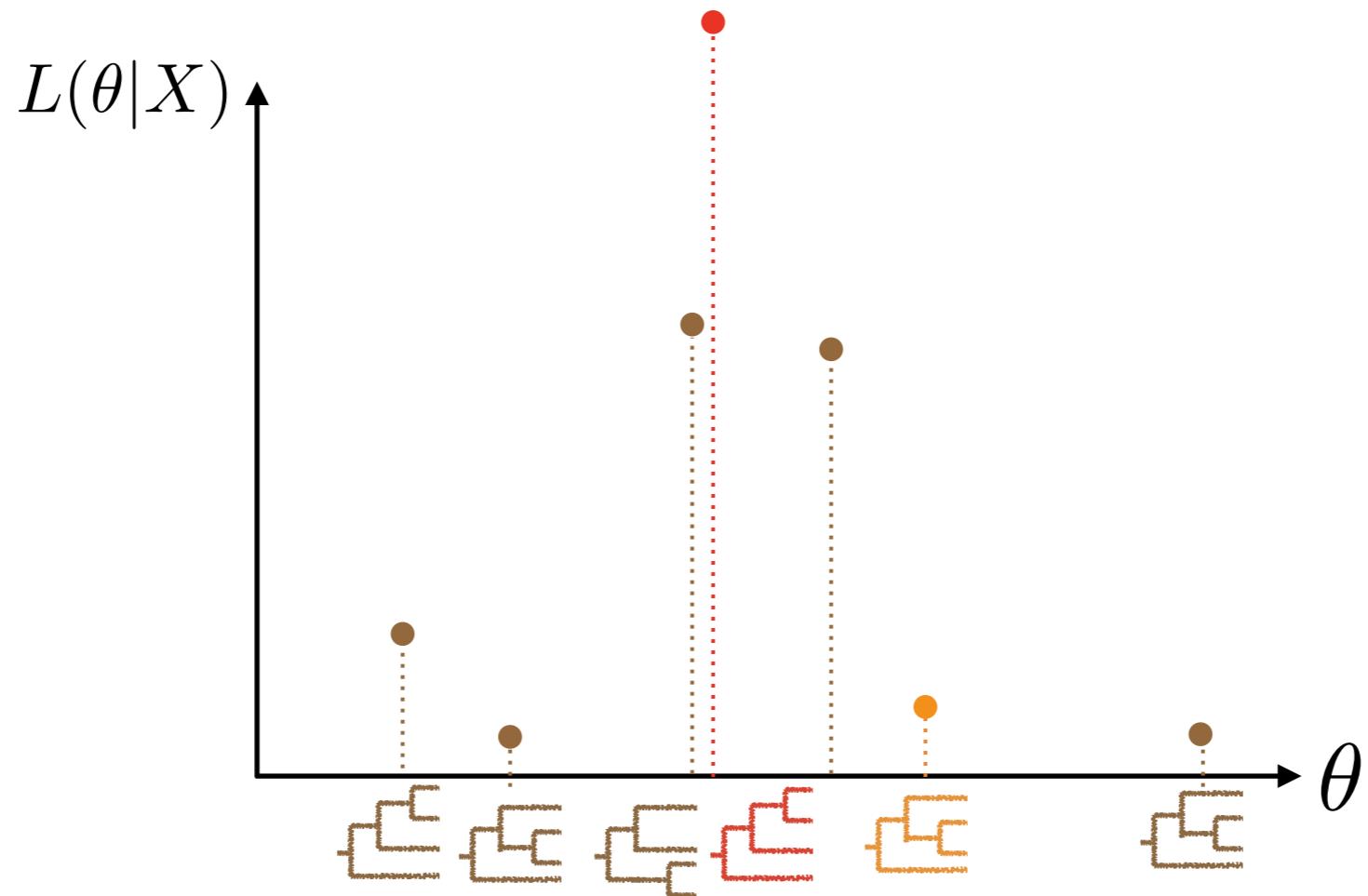
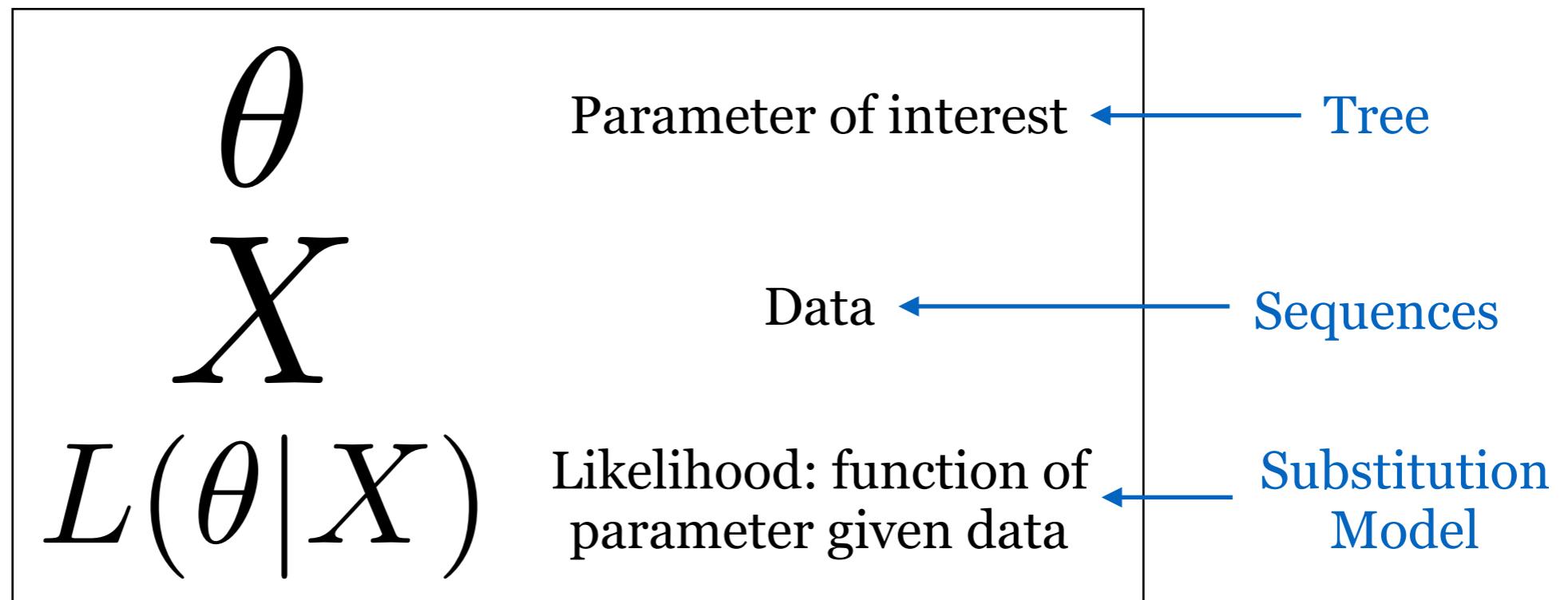
Example: maximum likelihood



Recap: maximum likelihood



Recap: maximum likelihood



Maximum likelihood recipe

Input: DNA sequences

Output: ML tree

1. Choose random starting tree: T_0
2. Calculate the likelihood of T_0 given the data: $L(T_0|X)$
3. Propose new tree T_1
4. Calculate the likelihood of new tree: $L(T_1|X)$
5. If $L(T_1|X) > L(T_0|X)$, keep T_1 ;
otherwise, keep T_0
6. Repeat

Maximum parsimony recipe

Input: DNA sequences

Output: MP tree

1. Choose random starting tree: T_0
2. Calculate the parsimony of T_0 given the data: $L(T_0|X)$
3. Propose new tree T_1
4. Calculate the parsimony of new tree: $L(T_1|X)$
5. If $L(T_1|X) > L(T_0|X)$, keep T_1 ;
otherwise, keep T_0
6. Repeat

Minimum evolution recipe

Input: DNA sequences

Output: ME tree

1. Choose random starting tree: T_0
2. Calculate the length of T_0 given the data:
3. Propose new tree $L(T_0|X)$
4. Calculate the length of new tree: T_1
5. If $L(T_1|X) < L(T_0|X)$, keep T_1 ; $L(T_1|X)$
otherwise, keep T_0
6. Repeat

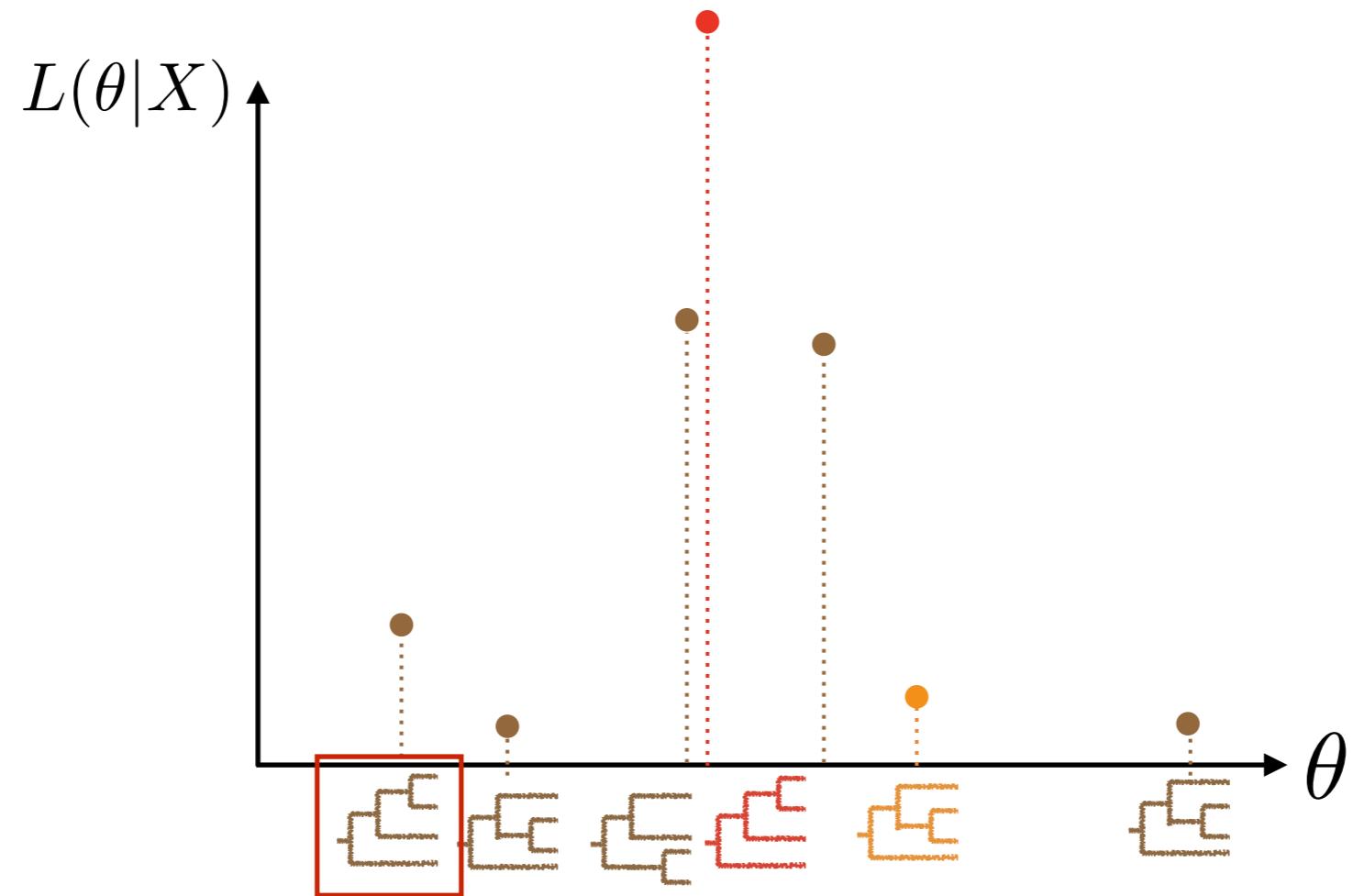
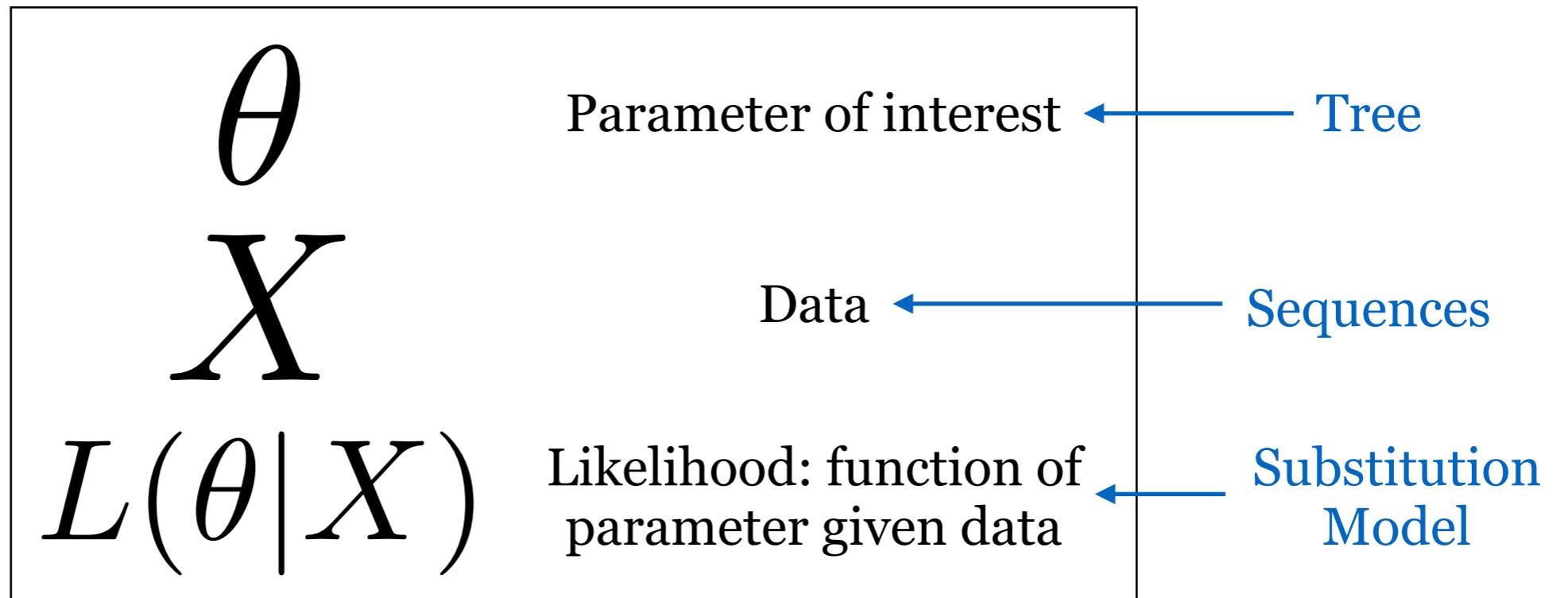
Phylogenetic inference

Step 1: Choose the criterion to use:
distances, parsimony, likelihood

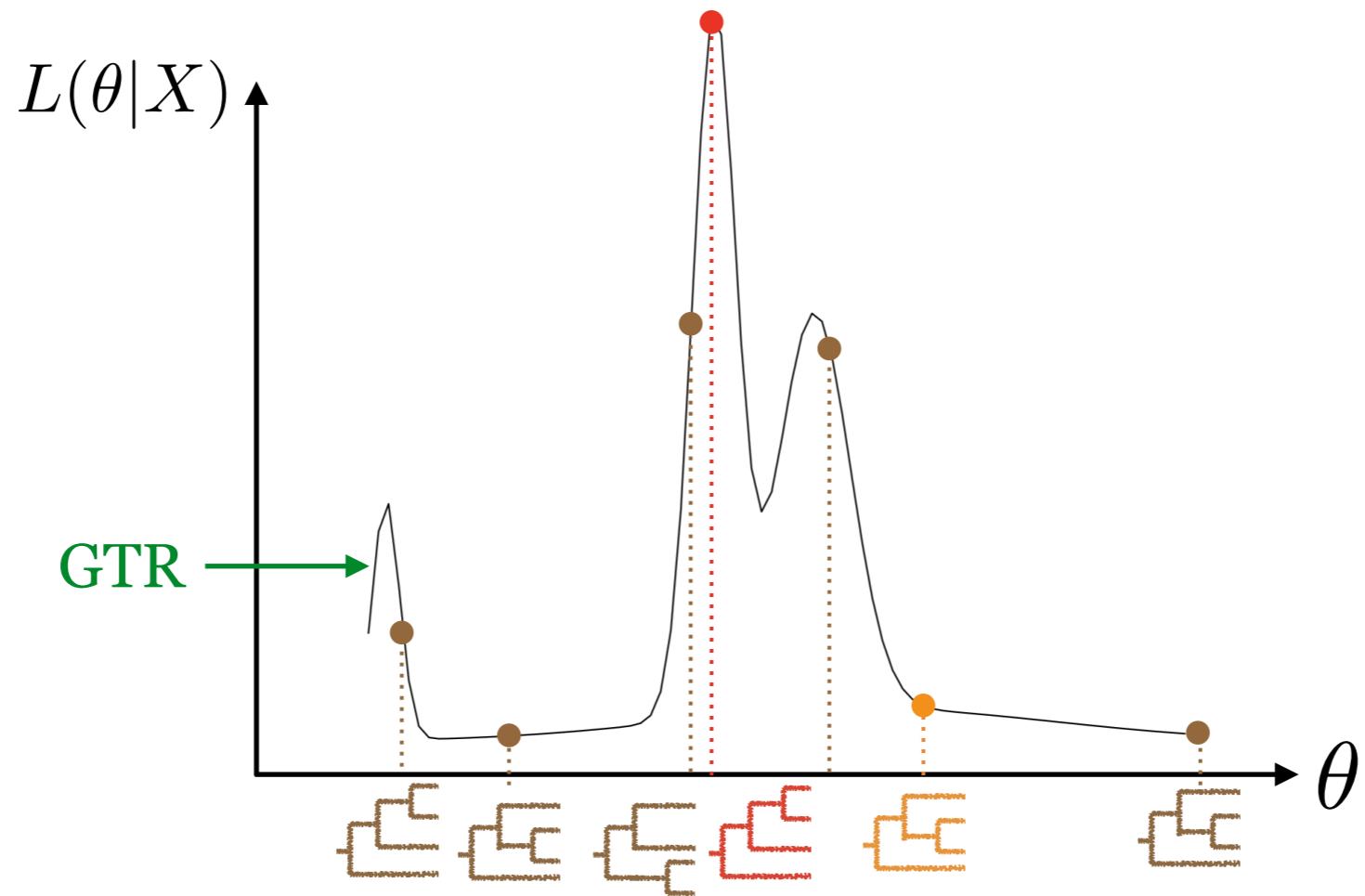
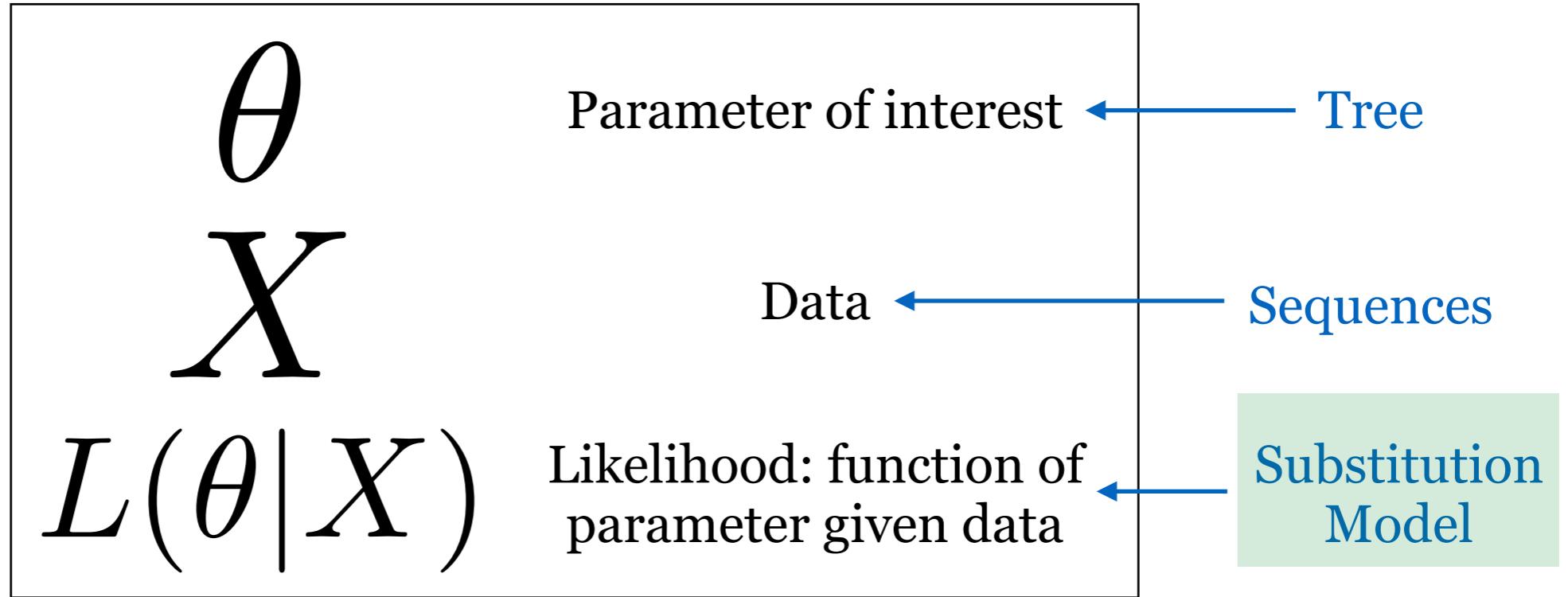
Step 2: Search the space of trees
until you find the optimum

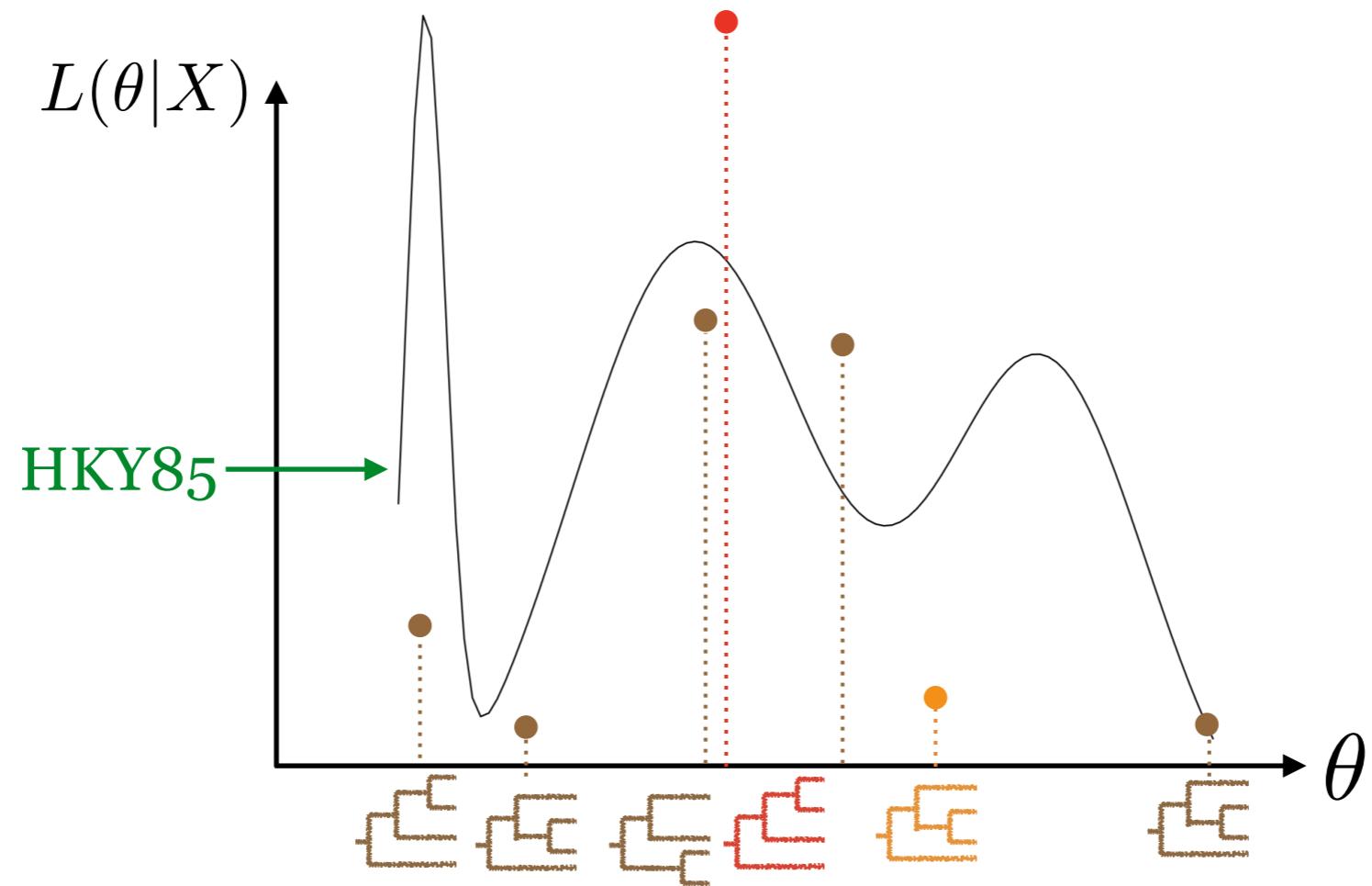
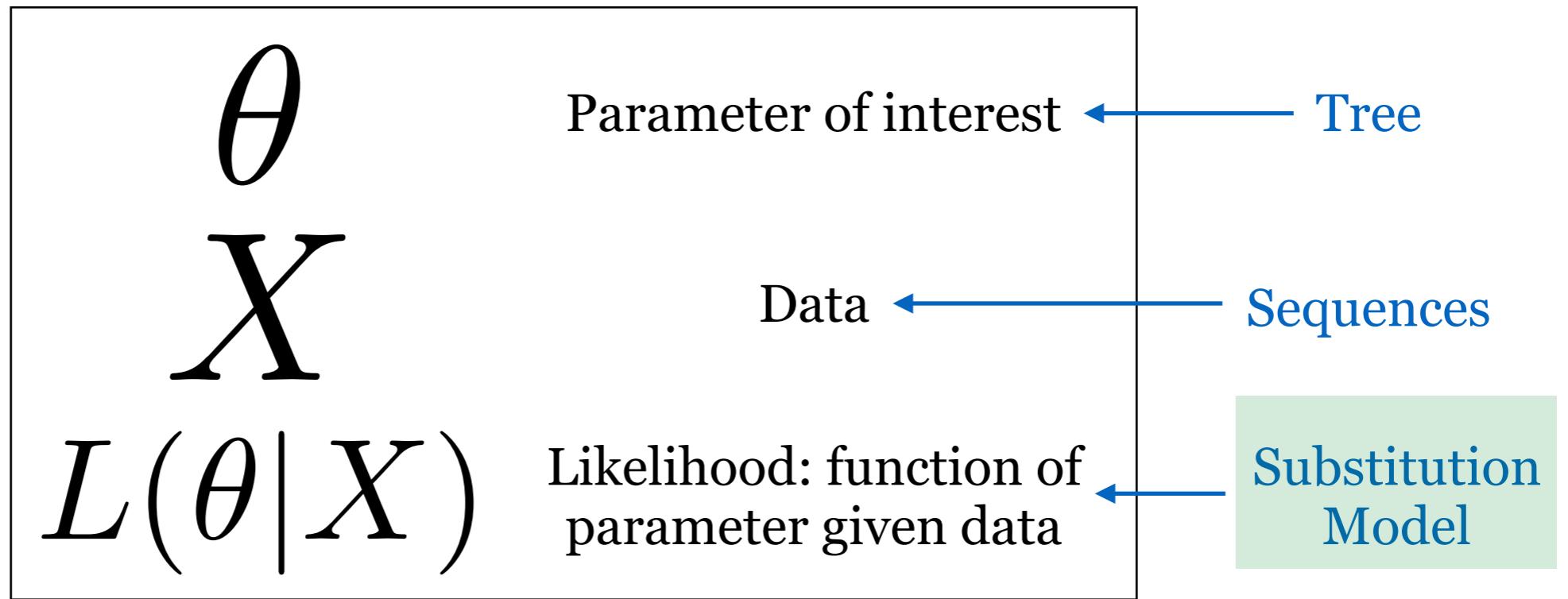
Weaknesses?

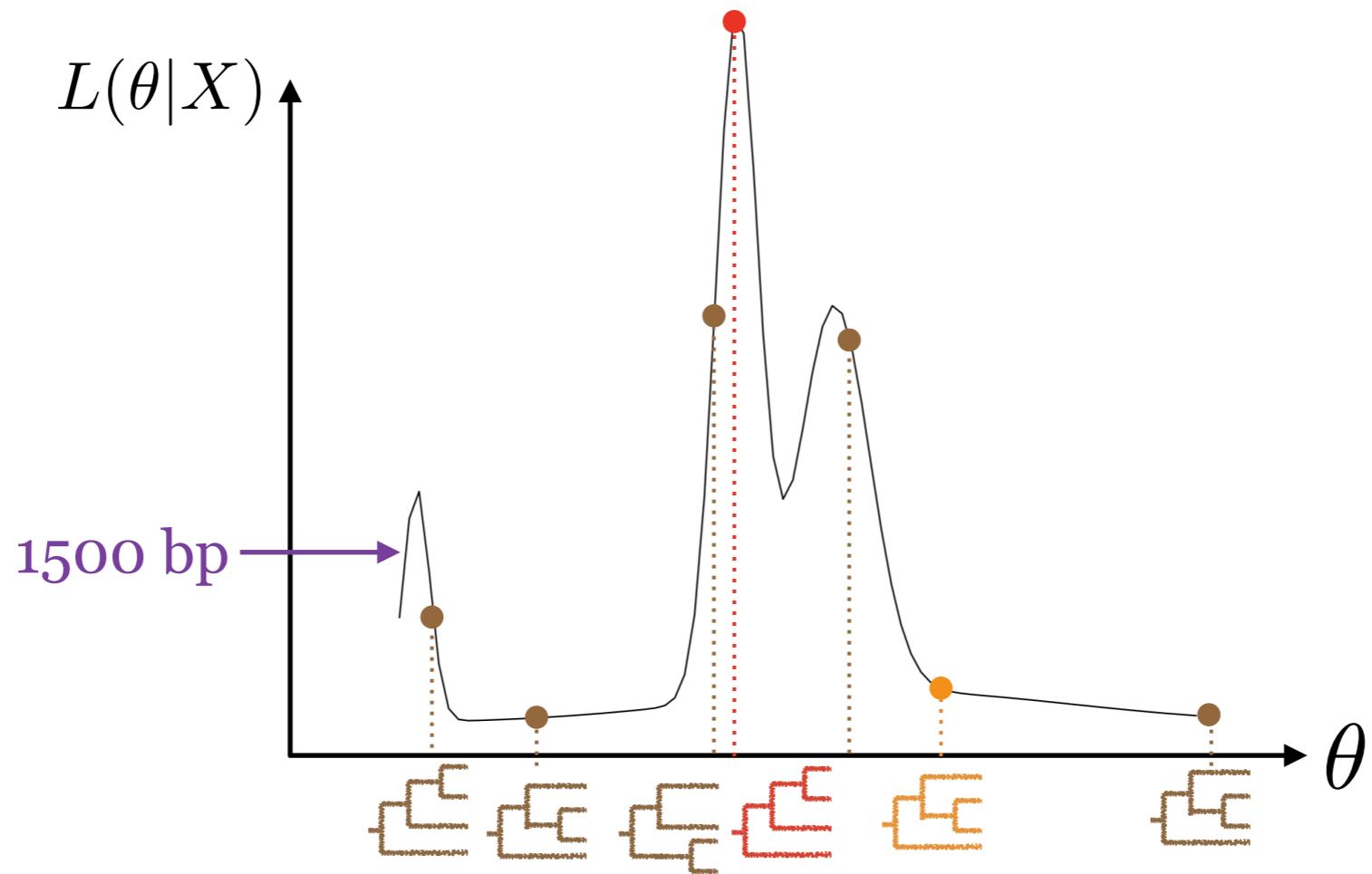
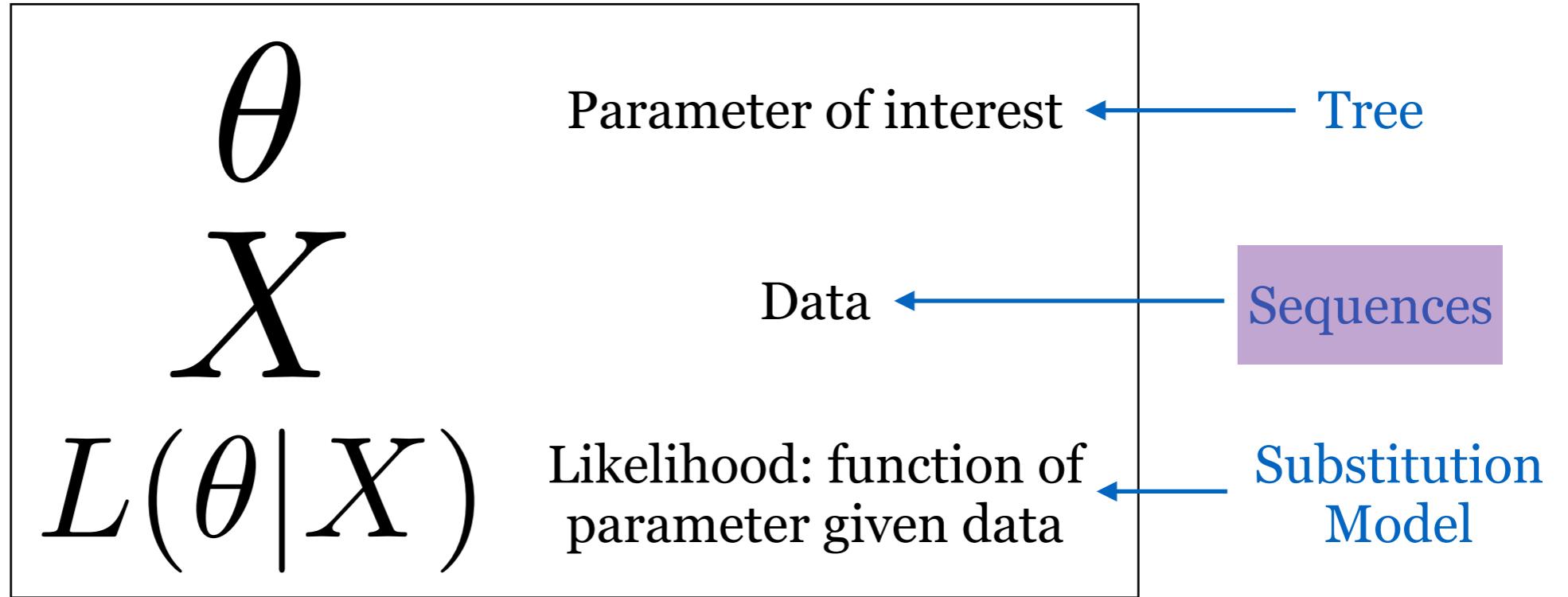


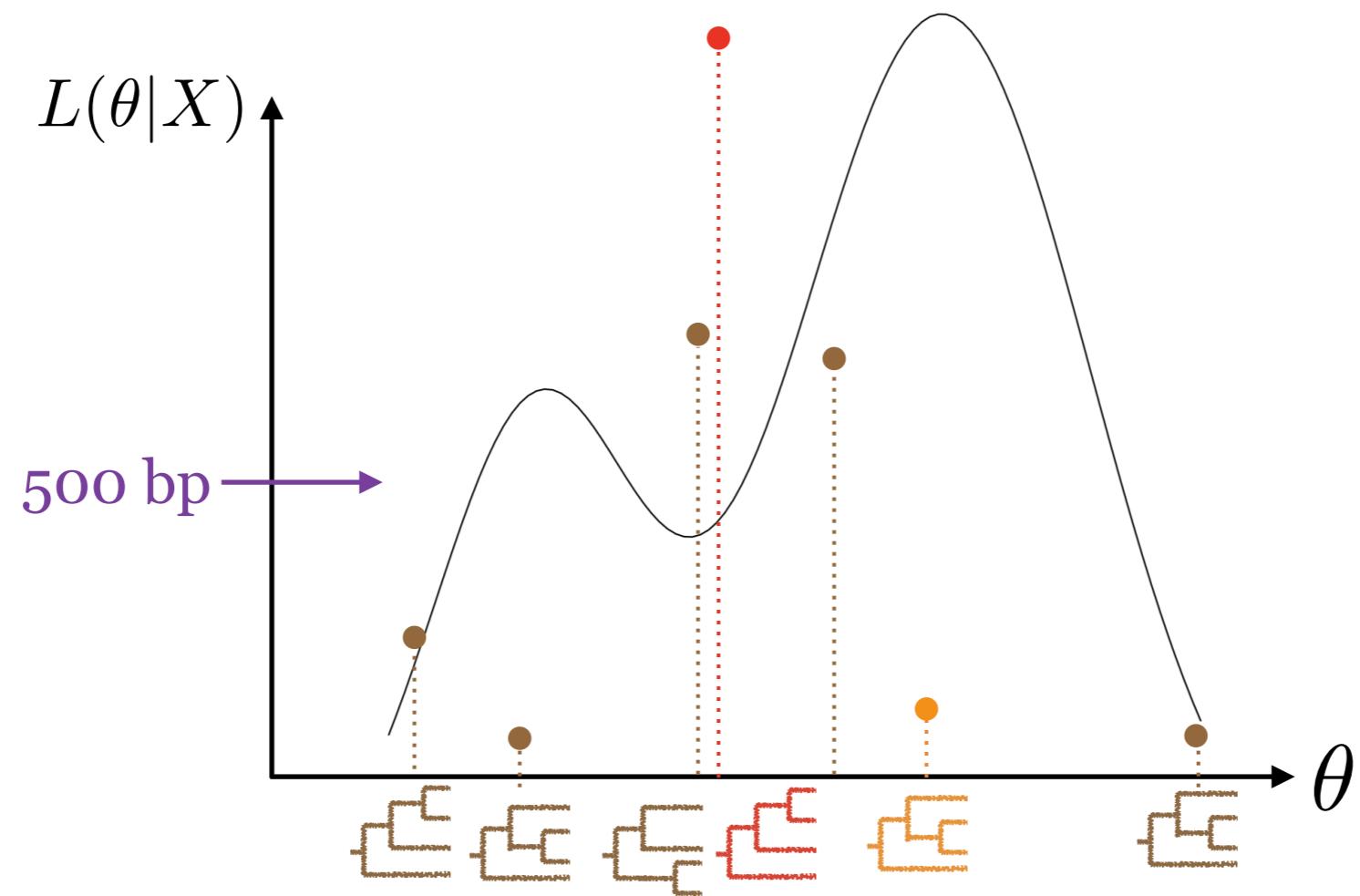
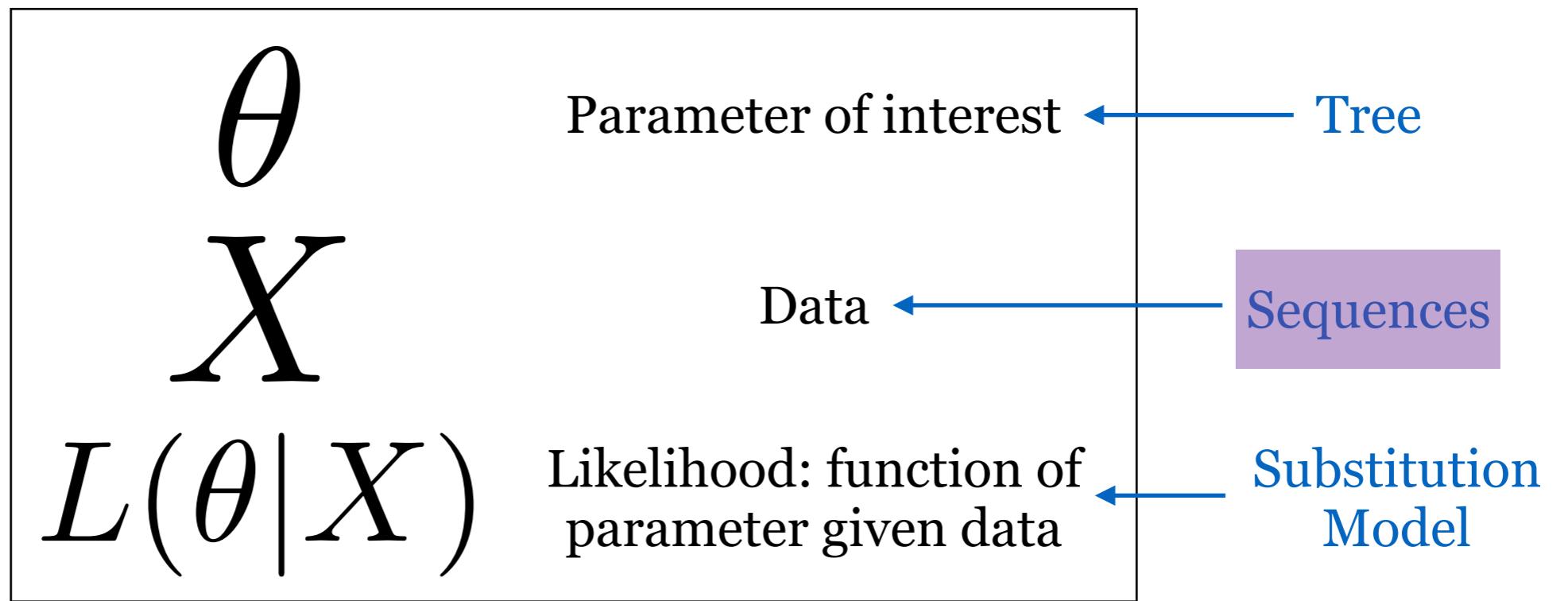


# Species	# Unrooted trees	# Rooted trees
1	1	1
2	1	1
3	1	3
4	3	15
5	15	105
6	105	945
7	945	10395
8	10,395	135,135
9	135,135	2,027,025
10	2,027,025	34,459,425
11	34,459,425	654,729,075
12	654,729,075	13,749,310,575
13	13,749,310,575	316,234,143,225
:	:	:
52	> # atoms in universe	









Sequences →

Phylogenetic inference

→ Tree

Well-chosen: ortholog
Perfectly aligned
Sample size
...
(talked about this already)

Criterion: distance,
parsimony, likelihood
Model selection: JC69,...
Convergence criteria
Model assumptions
...
(more in lecture 7-11)

Measures of confidence
(more in lecture 14)

# Species	# Unrooted trees	# Rooted trees
1	1	1
2	1	1
3	1	3
4	3	15
5	15	105
6	105	945
7	945	10395
8	10,395	135,135
9	135,135	2,027,025
10	2,027,025	34,459,425
11	34,459,425	654,729,075
12	654,729,075	13,749,310,575
13	13,749,310,575	316,234,143,225
:	:	:
52	> # atoms in universe	

RAxML

(Stamatakis, 2006)

Summary: RAxML-VI-HPC (randomized accelerated maximum likelihood for high performance computing) is a sequential and parallel program for inference of large phylogenies with maximum likelihood (ML). Low-level technical optimizations, a modification of the search algorithm, and the use of the GTR+CAT approximation as replacement for GTR+Γ yield a program that is between 2.7 and 52 times faster than the previous version of RAxML. A large-scale performance comparison with GARLI, PHYML, IQPNNI and MrBayes on real data containing 1000 up to 6722 taxa shows that RAxML requires at least 5.6 times less main memory and yields better trees in similar times than the best competing program (GARLI) on datasets up to 2500 taxa. On datasets ≥ 4000 taxa it also runs 2–3 times faster than GARLI. RAxML has been parallelized with MPI to conduct parallel multiple bootstraps and inferences on distinct starting trees. The program has been used to compute ML trees on two of the largest alignments to date containing 25 057 (1463 bp) and 2182 (51089 bp) taxa, respectively.

RAXML

(Stamatakis, 2006)

2 OPTIMIZATIONS OF RAXML

A detailed description of the optimizations listed below is provided in the on-line supplement. The main improvements cover:

- An efficient mechanism to store and re-store topologies and branch lengths via rearrangement descriptors.
- A consequent re-use of partial likelihood vectors.
- A dynamic adaptation of the rearrangement distance.
- Low-level optimization of the GTR+CAT and GTR+ Γ likelihood functions.
- An efficient re-implementation of Maximum Parsimony starting tree computations.

The datasets are described and available for public download (if permission has been granted by the authors) at diwww.epfl.ch/~stamatak (material frame). For each dataset 5 randomized MP starting trees have been computed with RAxML-VI-HPC.

RAXML

(Stamatakis, 2006)

Table 1. Alignment lengths in bp and number of distinct patterns/columns

# Taxa	# bp	# patterns	# Taxa	# bp	# patterns
1000	5547	3364	1497	1241	1241
1663	1577	1576	1728	1276	1275
2000	1251	1251	2560	1232	1232
4114	1263	1263	6722	1122	1122
7769	851	851	8780	1217	1217